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(54) Title: DNA SEQUENCES AND PLASMIDS FOR	THE	PR	EPARATION OF SUGAR BEET WITH CHANGED SUCROSE
CONCENTRATION			
(57) Abstract			
well as transgenic plants that by introduction of the DNA se	nicgrati	es e	in a plant genome of sugar beet change the sucrose concentration, as of the invention causes changes in sugar concentration.
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GA	Gabon				

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Title: <u>DNA sequences and plasmids for the preparation of sugar beet with changed sucrose concentration</u>

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### Field of the invention

The present invention relates to DNA sequences and plasmids, containing these DNA sequences, which by integration into the genome of a sugar-beet plant, changes the sugar metabolism of the plant to be changed. The invention also relates to transgenic plants formed with the help of these sequences.

Sucrose is of central importance for the plant and serves many functions. For the long distance transport of 15 photoassimilates and/or energy between various organs in clants, sucrose is almost exclusively used. The sucrose, which is transported in a specific heterotrophic organ, determines the growth and the development of this organ. Thus it is known, e.g. from EP 442 592, that transgenic 20 plants, in which the transport away of the sucrose from the exporting leaves is inhibited by expression of an apoplastic invertase, shows a strong reduction in the growth of e.g. roots or tubers in the case of potato plants. For tobacco plants, the principal importance of 25 sucrose as the central function for the long distance transport of energy carriers within the plant is described (von Schaewen et al, 1990, EMBO J 9: 3033-3044).

Further it is also known from EP 455 316 that DNA sequences present on plasmids, after introduction in a plant genome of a potato plant can affect the starch biosynthesis as well altering the amount and composition of the protein in the potato tubers.

Whilst it has known that a reduction of the amount of sucrose imported in the heterotrophic organs, such as tubers and seeds, leads to loss of yield, it is not known whether an increase in the amount of sucrose in the photosynthetically active parts of the plant, mainly the leaves, leads to a better supply of heterotrophic organs and thus to an increase in yield.

Besides sucrose and/or the hexoses, glucose and fructose,

derived from sucrose, have the property of protection of
plants against frost damage at low temperatures. Frost
damage is one of the main limiting factors in agricultural
productivity in the northern hemisphere. Temperatures
below freezing lead to the formation of ice crystals.

Since the growing ice crystals consist of pure water,
water is abstracted from the cells as the temperature

This dehydration has at least two potential damaging 20 results:

falls.

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- All dissolved substances within a cell are strongly concentrated and the cell contracts following the loss of water. Highly concentrated salts and organic acids lead to membrane damage.
- 2. With rehydration from dew, the previously contacted cells reexpand. The cell membrane also expands again. The volume expansion puts a heavy mechanical load on the membrane.
- It is thus clear that a freezing/dew cycle can lead to severe membrane damage of the cells and thus to damage to the plant.
- 35 It thus appears worth trying to hinder the freezing. One

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possible strategy is the increased formation of osmotically active substances in the cytosol of plant cells. This should lead to a lowering of the freezing point. Osmotically active substances include sucrose and/or the two hexoses derived from sucrose.

The increased formation of sucrose and/or the two hexoses at low temperatures is desirable in the growing plant. Another situation can exist in the harvested parts of a plant, especially in storage.

In relation to the economic aspects, sucrose thus possesses two especially important functions:

- as the transport form for the distant transport of photoassimilates,
- as an osmotically active substance with the desirable activity of lowering the freezing point in intact, growing plants.
- The biosynthesis pathways for the formation of sucrose, either from the primary photosynthesis products (in the leaf) or by breakdown of starch (in the storage organs e.g. of potatoes), are known.
- It is however, not known how and in what way changes of the carbohydrate concentration in sugar beet can be achieved since it is not possible to use even very similar genes such as for example genes that code for a sucrose synthase, ADP-glucose pyrophosphorylase or sucrose phosphate synthase of the potato with satisfactory success for the preparation of sugar beet with changed sucrose concentration. An exact analysis and determination of the DNA sequences or sequence fragments for the sugar beet is thus required.

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To change the sugar concentration in sugar beet, DNA sequences are now provided which code for the small and large subunit of the ADP glucose pyrophosphorylase, the sucrose synthase and the sucrose phosphate synthase of sugar beet (Seq. ID No 1-4).

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These DNA sequences can be introduced into plasmids and in this way combined with steering elements for expression in eukaryotic cells. Such steering elements are on the one hand transcription promoters and on the other hand transcription terminators. Each plasmid comprises:

- a) a suitable promoter which ensures that the coding sequence meets a suitable time point or in the specified developments in the transgenic plant or in determined genes of transgenic plants;
- b) at least a coding sequence for sugar beet that

  i) is so coupled to the promoter that the

  formation of an RNA is allowed which is into a

  protein, whereby the protein demonstrates an

  enzymatic activity which leads to a change of

  the sucrose concentration in the plant, or
  - ii) which is so coupled to the promoter that the coding part is read, which leads to the formation of a so-called anti-sense RNA which under-expresses the formation of the protein coded from an endogenous gene in the plant, that is involved in the sucrose biosynthesis; and
  - c) A non-coding termination sequence that contains the signal for the termination and polyadenylation of the transcript.

The coding sequences named under b) are the sequences that code for the large and small subunit of the ADP glucose pyrophosphorylase, for the sucrose phosphate synthase and for the sucrose synthase of sugar beet.

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The large subunit of the ADP-glucose-pyrophosphorylase has the following nucleotide sequence (Seq. ID No. 1):

CAA	AAGA	AAA A	ACTT	CCCA	TT TO	CTAC:	TTCT	r TG	CACA	TAT	AAT	TTCC	CAC		0050
CAAT	TTTT:	rcr :	LAATT	ATTT	CT C	ACTT	rcat:	r ta	ATCAC	STTT	TCAG	GCAA	CAT		0100
TCT	GATA	CTC (	GACA	ACCC	AC T	TCT	STTC	r cc	CAAG	ATTC	CAAJ	ACCT	CTG		0150
ATTO	CTCA!	TTC (	CACT	AATA	rt ti	rtgci	TAT:	r TT	TTTT	CTGG	ATT	CAAA	SAA		0200
AAG													CC C		0243
	Me	et As	sp A	la Se	er A.		la Al	la I	le As	sn Va	al As	sn Al	la Hi	s	
						5				1	LO				
መመን	አ ር አ	CAA	ሮጥጥ	GG A	AAG	444	CGT	արդուր	ጥጥ አ	GGA	GAG	AGA	ATC	AGT	0288
													Ile		
Deu	15	GIU	V 4 1	O ± y	270	20	9			1	25	5			
	10														
CAA	AGT	TTG	AAG	GGT	AAA	GAT	CTG	AGA	GCT	CTG	TTT	TCA	AGA	ACT	0333
Gln	Ser	Leu	Lys	Gly	Lys	Asp	Leu	Arg	Ala	Leu	Phe	Ser	Arg	Thr	
	30					35					40				
														TCT	0378
Glu	Ser	Lys	Gly	Arg	Asn	Val	Asn	Lys	Pro	Gly	Val	Ala	Phe	Ser	
	45					50					55				
														AAA	0423
Val		Thr	Ser	Asp	Phe		Gln	Ser	Val	Lys		Ser	Leu	rys	
	60					65					70				

TAT	GAG	CCA	GCA	TTA	TTT	GAA	TCT	CCA	AAA	GCT	GAC	CCA	AAA	TAA	0468
Tyr	Glu	Pro	Ala	Leu	Phe	Glu	Ser	Pro	Lys	Ala	Asp	Pro	Lys	Asn	
	75					80					85			•	
GTG	GCT	GCA	ATT	GTG	CTG	GGT	GGT	GGT	GCT	GGG	ACT	CGC	CTC	TTT	0513
Val	Ala	Ala	Ile	Val	Leu	Gly	Gly	Gly	Ala	Gly	Thr	Arg	Leu	Phe	
	90					95					100				
CCT	CTT	ACT	AGC	AGG	AGA	GCT	AAG	CCA	GCA	GTG	CCA	ATT	GGA	GGG	0558
Pro	Leu	Thr	Ser	Arg	Arg	Ala	Lys	Pro	Ala	Val	Pro	Ile	Gly	Gly	
	105					110					115				
TGT	TAC	AGG	CTG	ATT	GAT	GTG	CCT	ATG	AGC	AAC	TGC	ATC	AAC	AGT	0603
Cys	Tyr	Arg	Leu	Ile	Asp	Val	Pro	Met	Ser	Asn	Cys	Ile	Asn	Ser	
	120					125					130				
	•														
GGC	ATT	AGA	AAG	ATT	TTC	ATT	CTT	ACC	CAG	TTC	AAT	TCG	TTT	TCG	0648
Gly	Ile	Arg	Lys	Ile	Phe	Ile	Leu	Thr	Gln	Phe	Asn	Ser	Phe	Ser	
	135					140	•				145				
CTT	AAT	CGT	CAT	CTT	GCT	CGA	ACC	TAT	AAT	TTT	GGA	GAT	GGT	GTG	0693
Leu	Asn	Arg	His	Leu	Ala	Arg	Thr	Tyr	Asn	Phe	GJA	Asp	Gly	Val	
	150					155					160				
AAT	TTT	GGG	GAT	GGC	TTT	GTG	GAG	GTT	TTT	GCT	GCT	ACA	CAA	ACA	0738
Asn	Phe	Gly	Asp	Gly	Phe	Val	Glu	Val	Phe	Ala	Ala	Thr	Gln	Thr	
	165					170					175				

CCT	GGA	GAA	TCA	GGA	AAG	AAA	TGG	TTC	CAG	GGC	ACC	GCT	GAT	GCA	0783
Pro	Gly	Glu	Ser	Gly	Lys	Lys	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ala	
	180					185					190			•	
GTA	AGA	CAG	TTT	TTC	TGG	GCA	TTT	GAG	GAT	TCC	AAA	TCC	AAG	GAT	0828
Val	Arg	Gln	Phe	Phe	Trp	Ala	Phe	Glu	Asp	Ser	Lys	Ser	Lys	Asp	
	195					200					205				
GTC	GAG	CAT	ATA	GTT	ATT	TTA	TCC	GGT	GAT	CAT	CTT	TAC	CGA	ATG	0873
Val	Glu	His	Ile	Val	Ile	Leu	Ser	Gly	Asp	His	Leu	Tyr	Arg	Met	
	210					215					220				
GAT	TAC	ATG	AGT	TTT	TGG	CAG	AAG	CAC	ATT	GAC	ACC	AAT	GCT	GAT	0918
Asp	Tyr	Met	Ser	Phe	Trp	Gln	Lys	His	Ile	Asp	Thr	Asn	Ala	Asp	
	225					230					235				
ATT	ACA	GTG	TCA	TGC	ATA	CCC	ATG	GAT	GAC	AGC	CGT	GCA	TCG	GAT	0963
Ile		Val	Ser	Cys			Met	Asp	Asp		_	Ala	Ser	Asp	
	240					245					250				
		CTG													1008
Tyr	_	Leu	Met	Lys			His	Thr	GIY			Val	HIS	Pne	
	255					260					265				
	<b>63.3</b>		000	220	CCTT	·mom	C እ m	CULY	7 (7 )	CCN	አጥሮ	C	CTD	CAT	1053
		AAA													1023
Ala		Lys	PLO	гìя	GIÀ		мыр	Dea	THE	WIG	280	GIN	vaı	wsh	
	270					275					280				

									GAA						1098
Thr	Thr	Val	Leu	Gly	Leu	Ser	Asp	Leu	Glu	Ala	Met	Ser	Asn	Pro	
	285					290					295			•	
TAT	ATT	GCA	TCA	ATG	GGT	GTT	TAT	GTC	TTT	CGA	ACG	GAT	GTT	CTT	1143
Tyr	Ile	Ala	Ser	Met	Gly	Val	Tyr	Val	Phe	Arg	Thr	Asp	Val	Leu	
-	300					305					310				
ATG	GAG	CTT	CTC	AAT	CGA	AAA	TAC	CCT	TCA	AGC	AAT	GAT	TTT	GGC	1188
Met	Glu	Leu	Leu	Asn	Arg	Lys	Tyr	Pro	Ser	Ser	Asn	Asp	Phe	Gly	
	315					320					325				
TCT	GAG	ATT	ATT	CCT	TCA	GCT	GTA	GGA	GAG	TCT	AAT	GTT	CAG	GCA	1233
Ser	Glu	Ile	Ile	Pro	Ser	Ala	Val	Gly	Glu	Ser	Asn	Val	Gln	Ala	
	330					335					340				
-															
									ATC						1278
Tyr									ATC Ile						1278
Tyr															1278
	Leu 345	Phe	Asn	Asp	Tyr	Trp 350	Glu	Asp	Ile	Gly	Thr 355	Ile	Lys	Ser	1278
TTC	Leu 345 TTT	Phe GAT	Asn TCC	Asp AAT	Tyr TTG	Trp 350 GCC	Glu CTT	Asp ACA	Ile	Gly CAG	Thr 355 CCT	Ile	Lys AAG	Ser TTT	1278
TTC	Leu 345 TTT	Phe GAT	Asn TCC	Asp AAT	Tyr TTG	Trp 350 GCC	Glu CTT	Asp ACA	Ile	Gly CAG	Thr 355 CCT	Ile	Lys AAG	Ser TTT	
TTC	Leu 345 TTT	Phe GAT	Asn TCC	Asp AAT	Tyr TTG	Trp 350 GCC	Glu CTT	Asp ACA	Ile	Gly CAG	Thr 355 CCT	Ile	Lys AAG	Ser TTT	
TTC	Leu 345 TTT Phe	Phe GAT	Asn TCC	Asp AAT	Tyr TTG	Trp 350 GCC Ala	Glu CTT	Asp ACA	Ile	Gly CAG	Thr 355 CCT Pro	Ile	Lys AAG	Ser TTT	
TTC Phe	Leu 345 TTT Phe 360	Phe GAT Asp	Asn TCC Ser	Asp AAT Asn	Tyr TTG Leu	Trp 350 GCC Ala 365	Glu CTT Leu	Asp ACA Thr	Ile CAA Gln	Gly CAG Gln	Thr 355 CCT Pro 370	Ile CCC Pro	Lys AAG Lys	Ser TTT Phe	1323
TTC Phe	Leu 345 TTT Phe 360	Phe GAT Asp	TCC Ser	ASP AAT ASN	TYT TTG Leu	Trp 350 GCC Ala 365	CTT Leu	Asp ACA Thr	CAA Gln	CAG Gln ACA	Thr 355 CCT Pro 370	CCC Pro	Lys AAG Lys	TTT Phe	
TTC Phe	Leu 345 TTT Phe 360	Phe GAT Asp	TCC Ser	ASP AAT ASN	TYT TTG Leu	Trp 350 GCC Ala 365	CTT Leu	Asp ACA Thr	Ile CAA Gln	CAG Gln ACA	Thr 355 CCT Pro 370 TCT Ser	CCC Pro	Lys AAG Lys	TTT Phe	1323
TTC Phe	Leu 345 TTT Phe 360	Phe GAT Asp	TCC Ser	ASP AAT ASN	TYT TTG Leu	Trp 350 GCC Ala 365	CTT Leu	Asp ACA Thr	CAA Gln	CAG Gln ACA	Thr 355 CCT Pro 370	CCC Pro	Lys AAG Lys	TTT Phe	1323

CTG	CCT	CCT	ACA	AAA	GTC	GAC	AGG	TGC	AAG	ATT	GTC	GAT	TCC	ATT	1413
Leu	Pro	Pro	Thr	Lys	Val	Asp	Arg	Cys	Lys	Ile	Val	Asp	Ser	Ile	
	390					395					400			•	
											ATC				1458
Val		His	Gly	Cys	Phe		Gln	Glu	Ser	Ser	Ile	Gln	His	Ser	
	405					410					415				
							<b></b>	<b></b>	<b></b>					•••	
											GTT				1503
TTE		GIŸ	val	Arg	Ser	_	Leu	GIU	Ser	GIY	Val	GIu	Phe	GIn	
	420					425					430				
GAC	ACC	ATG	ATG	ATG	GGC	GCA	GAT	TAC	TAT	CAA	ACT	GAA	TCA	GAA	1348
											Thr				
•	435				-	440	•	-	•		445				
ATT	GCT	TCT	CTG	CTT	GCT	GAG	GGA	AAG	GTT	CCT	GTT	GGT	GTC	GGA	1593
Ile	Ala	Ser	Leu	Leu	Ala	Glu	Gly	Lys	Val	Pro	Val	Gly	Val	Gly	
	450					455					460				
											AAG				1638
Gln		Thr	Lys	Ile			Cys	Ile	Ile		Lys	Asn	Ala	Lys	
	465					470					475				
<b>.</b>			<b>63.</b> T	CMC	C TL N	እሙሩ	CC3	220	200	C N ID	ccm	C TO TO	CAC	C	1600
											GGT				1683
тте	GIY	тЛг	ASP	val		116	WIG	Abli	THE		Gly	val	GIU	GIU	

GCA GAT AGA CCA AAT GAA GGC TTT TAC ATC AGG TCG GGC ATT ACC Ala Asp Arg Pro Asn Glu Gly Phe Tyr Ile Arg Ser Gly Ile Thr 495 500 505	
ATC ATT TTG AAG AAC GCA ACC ATA CAA GAC GGT CTT GTG ATT TAG  Ile Ile Leu Lys Asn Ala Thr Ile Gln Asp Gly Leu Val Ile End  510 515 520	
ATTTAATCAT AACCTCATTA GAAAGAAATA ATTTTGCATG ATTTCCTTTT	1823
CATGTAACCT AAACTGGCTA AACCACGAGG TTTTCTCATC TGTATATATA	1873
ATATGTCTAT AACTATGGAT AATCTTAATA AAAAAAAAA AAAAAAAAA	1923
A	1924
The small subunit of the ADP-glucose-pyrophosphalase h the following nucleotide sequence (Seq. ID No. 2):	as
GG ATA ACT GTG CCA TCA ACC TCC TCA AAG AAC CTC CAA AAT AGC	0044
Ile Thr Val Pro Ser Thr Ser Ser Lys Asn Leu Gln Asn Ser 5 10	
CTC GCA TTC TCC TCT TCT TCT CTC TCC GGC GAC AAA ATT CAA ACG	0089
Leu Ala Phe Ser Ser Ser Leu Ser Gly Asp Lys Ile Gln Thr	
15 20 25	
	0134
15 20 25	0134

CCG	ATT	GTT	GTC	TCT	CCC	AAA	GCT	GTT	TCT	GAT	TCT	AAG	AAT	TCG	0179
Pro	Ile	Val	Val	Ser	Pro	Lys	Ala	Val	Ser	Asp	Ser	Lys	Asn	Ser	
45					50					55					
CAG	ACT	TGT	CTT	GAC	CCT	GAA	GCC	AGC	CGT	AGT	GTT	CTT	GGT	ATT	0224
Gln	Thr	Cys	Leu	Asp	Pro	Glu	Ala	Ser	Arg	Ser	Val	Leu	Gly	Ile	
60					65					70					
ATA	CTT	GGA	GGT	GGT	GCT	GGT	ACA	CGT	CTT	TAC	CCG	TTG	ACT	AAG	0269
Ile	Leu	Gly	Gly	Gly	Ala	Gly	Thr	Arg	Leu	Tyr	Pro	Leu	Thr	Lys	
75					80					85					
												•			
AAG	AGA	GCC	AAA	CCA	GCC	GTG	CCA	CTC	GGT	GCT	AAT	TAT	AGG	CTT	0314
Lys	Arg	Ala	Lys	Pro	Ala	Val	Pro	Leu	Gly	Ala	Asn	Tyr	Arg	Leu	
90					95					100					
TTA	GAT	ATC	CCA	GTG	AGC	TAA	TGT	TTG	AAC	AGT	AAT	ATT	TCC	AAA	0359
Ile	Asp	Ile	Pro	Val	Ser	Asn	Cys	Leu	Asn	Ser	Asn	Ile	Ser	Lys	
105					110					110					
ATA	TAT	GTT	CTT	ACA	CAA	TTC	AAT	TCT	GCT	TCT	CTG	AAT	CGT	CAT	0404
Ile	Tyr	Val	Leu	Thr	Gln	Phe	Asn	Ser	Ala	Ser	Leu	Asn	Arg	His	
115					120					125					
CTT	TCG	CGG	GCA	TAT	GCT	AGC	AAC	ATG	GGA	GGA	TAC	AAA	AAT	GAG	0449
Leu	Ser	Arg	Ala	Tyr	Ala	Ser	Asn	Met	Gly	Gly	Tyr	Lys	Asn	Glu	
130					135					140					
						•									
GGG	$\mathbf{T}\mathbf{T}\mathbf{T}$	GTA	GAA	GTT	CTT	GCT	GCT	CAG	CAA	AGT	CCA	GAG	TAA	CCA	0494
Sly	Phe	Val	Glu	Val	Leu	Ala	Ala	Gln	Gln	Ser	Pro	Glu	Asn	Pro	
145					150					155					

AAC	TGG	TTT	CAG	GGT	ACA	GCT	GAT	GCT	GTT	AGG	CAA	TAT	CTG	TGG	0539
Asn	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ala	Val	Arg	Gln	Tyr	Leu	Trp	
160					165					170					
CTT	TTC	GAA	GAG	CAC	AAT	GTT	CTT	GAG	TAC	TTG	ATT	CTT	GCT	GGT	0584
Leu	Phe	Glu	Glu	His	Asn	Val	Leu	Glu	Tyr	Leu	Ile	Leu	Ala	Gly	
175					180					185					
		•													
GAC	CAT	TTG	TAT	CGA	ATG	GAT	TAT	GAA	AGA	TTT	GTC	CAA	GCT	CAC	0629
Asp	His	Leu	Tyr	Arg	Met	Asp	Tyr	Glu	Arg	Phe	Val	Gln	Ala	His	
190			-	•	195	_	_		_	200					
			٠.												
AGA	GAA	ACT	GAT	GCA	GAC	ATT	ACT	GTT	GCT	GCA	TTG	CCA	ATG	GAT	0674
					Asp										
205			-		210					215					
GAA	AAG	CGT	GCT	ACT	GCA	TTT	GGT	TTG	ATG	AAA	ATT	GAT	GAA	GAA	0719
Glu	Lys	Arg	Ala	Thr	Ala	Phe	Gly	Leu	Met	Lys	Ile	Asp	Glu	Glu	
220	-	_			225					230					
GGA	AGA	ATT	ATT	GAG	TTT	GCC	GAG	AAA	CCG	AAA	GGA	GAA	CAA	TTG	0764
Gly	Arq	Ile	Ile	Glu	Phe	Ala	Glu	Lys	Pro	Lys	Gly	Glu	Gln	Leu	
235	,				240					245	_				
AAA	GCT	ATG	AAG	GTT	GAT	ACC	ACA	ATC	CTG	GGT	CTG	GAC	GAT	GAG	0809
					Asp										
250			4		255					260		-	-		

AGA	GCA	AAA	GAA	ATG	CCA	TTC	ATA	GCC	AGC	ATG	GGC	ATA	TAT	GTT	085
Arg	Ala	Lys	Glu	Met	Pro	Phe	Ile	Ala	Ser	Met	Gly	Ile	Tyr	Val	
265					270					275				•	
ATT	AGC	AAA	GAT	GTA	ATG	CTT	AAT	CTG	CTT	CGG	GAG	CAA	TTT	CCT	0899
Ile	Ser	Lys	Asp	Val	Met	Leu	Asn	Leu	Leu	Arg	Glu	Gln	Phe	Pro	
280		_			285					290					
GGT	GCT	AAT	GAT	TTT	GGA	AGT	GAA	GTT	ATT	CCA	GGC	GCC	ACT	TCC	0944
										Pro					
295			•		300					305	-				
							٠.								
ATA	GGG	TTG	AGA	GTC	CAA	GCT	TAT	TTG	TAT	GAT	GGT	TAC	TGG	GAG	0989
Ile	Gly	Leu	Arg	Val	Gln	Ala	Tyr	Leu	Tyr	Asp	Gly	Tyr	Trp	Glu	
310	-				315		-		-	320	_	-			
GAT	ATT	GGT	ACC	ATT	GAA	GCT	TTT	TAC	AAT	GCT	AAC	TTG	GGA	ATC	1034
Asp	Ile	Gly	Thr	Ile	Glu	Ala	Phe	Tyr	Asn	Ala	Asn	Leu	Gly	Ile	
325		_			330					335					
ACC	AAA	AAG	CCG	GTG	CCA	GAT	TTT	AGC	TTC	TAT	GAT	CGT	TCA	TCT	1079
Thr	Lys	Lys	Pro	Val	Pro	Asp	Phe	Ser	Phe	Tyr	Asp	Arg	Ser	Ser	
340	_				345					350					
CCA	ATT	TAT	ACA	CAA	CCT	CGG	TAT	TTG	CCT	CCT	TCA	AAG	ATG	CTT	1124
Pro	Ile	Tyr	Thr	Gln	Pro	Arg	Tyr	Leu	Pro	Pro	Ser	Lys	Met	Leu	
355		-			360					365					

GAI	GCT	GAT	ATA	ACT	GAC	AGC	GTC	ATC	GGT	GAA	GGC	TGT	GTT	ATT	1169
Asp	Ala	Asp	Ile	Thr	Asp	Ser	Val	Ile	Gly	Glu	Gly	Cys	Val	Ile	
370					375					380					
AAG	AAC	TGT	AAG	ATT	CAT	CAT	TCT	GTT	ATC	GGA	CTT	CGA	TCT	TGT	1214
Lys	Asn	Cys	Lys	Ile	His	His	Ser	Val	Ile	Gly	Leu	Arg	Ser	Cys	
385		_	_		390					395					
ATC	TCG	GAG	GGT	GCA	ATC	ATT	GAG	GAC	ACA	CTG	TTG	ATG	GGA	GCT	1259
										Leu					
400			-		405			-		410			_		
GAT	TAT	TAT	GAG	ACT	GAT	GCT	GAT	CGG	AAA	TTC	CTG	GCT	GCT	AAG	1304
										Phe					
	-														
415					420					425					
415					420					425					
415					420					425					
	AGT	GTA	CCT	ATT		ATT	GGG	AAT	GCA	425 CGT	ATT	GGG	GAT	GAT	1349
GGT					GGA										1349
GGT Gly					GGA				Ala	CGT					1349
GGT					GGA Gly				Ala	CGT Arg					1349
GGT Gly					GGA Gly				Ala	CGT Arg					1349
GGT Gly 430	Ser	Val	Pro	Ile	GGA Gly 435	Ile	Gly	Asn	Ala	CGT Arg 440	I <u>l</u> e	Gly	Asp	Asp	1349
GGT Gly 430 GTC	Ser AAG	Val	Pro ATC	Ile AAC	GGA Gly 435	Ile GAC	Gly AAT	Asn GTA	Ala CAA	CGT Arg 440 GAA	I <u>le</u>	Gly GCA	Asp AGA	Asp GAA	
GGT Gly 430 GTC Val	Ser AAG	Val	Pro ATC	Ile AAC	GGA Gly 435	Ile GAC	Gly AAT	Asn GTA	Ala CAA Gln	CGT Arg 440	I <u>le</u>	Gly GCA	Asp AGA	Asp GAA	
GGT Gly 430 GTC	Ser AAG	Val	Pro ATC	Ile AAC	GGA Gly 435 AGT Ser	Ile GAC	Gly AAT	Asn GTA	Ala CAA Gln	CGT Arg 440 GAA Glu	I <u>le</u>	Gly GCA	Asp AGA	Asp GAA	
GGT Gly 430 GTC Val	Ser AAG	Val	Pro ATC	Ile AAC	GGA Gly 435 AGT Ser	Ile GAC	Gly AAT	Asn GTA	Ala CAA Gln	CGT Arg 440 GAA Glu	I <u>le</u>	Gly GCA	Asp AGA	Asp GAA	
GGT Gly 430 GTC Val 445	Ser AAG Lys	Val ATT Ile	Pro ATC Ile	Ile AAC Asn	GGA Gly 435 AGT Ser 450	Ile GAC Asp	Gly AAT Asn	Asn GTA Val	Ala CAA Gln	CGT Arg 440 GAA Glu	Ile GCA Ala	Gly GCA Ala	Asp AGA Arg	Asp GAA Glu	
GGT Gly 430 GTC Val 445	AAG Lys GAC	Val ATT Ile	Pro ATC Ile	Ile AAC Asn	GGA Gly 435 AGT Ser 450	GAC Asp	Gly AAT Asn	Asn GTA Val	Ala CAA Gln ATA	CGT Arg 440 GAA Glu 455	Ile GCA Ala	GCA Ala	ASP AGA Arg	GAA Glu AAG	1394
GGT Gly 430 GTC Val 445	AAG Lys GAC	Val ATT Ile	Pro ATC Ile	Ile AAC Asn	GGA Gly 435 AGT Ser 450	GAC Asp	Gly AAT Asn	Asn GTA Val	CAA Gln ATA Ile	CGT Arg 440 GAA Glu 455	Ile GCA Ala	GCA Ala	ASP AGA Arg	GAA Glu AAG	1394

	1482
Asp Ala Met Ile Pro Ser Gly Thr Val Ile End	
475 480 485	•
·	
TATAATAAAT ATCACTGCCT ATTTACAGTA CCTATCTGAG TCTCCCACCA	1532
TGACCCTTTG ATTCAATCTT TTAGTTATGT AAATATTTTT GGCTTTTGCG	1582
ATTTTGCCAT AAATTTGAAG AAGCGAGGAT TCAGGGACGA TAGTGCTATG	1632
AATTGGAAGA AAGGATTTGG GGGATATCTT TGTAAAGACA TTTTGACTAC	1682
TGGGCACTAA AAATTTGGTA ATGCTATACC AAAATATATA AAAAGATCTT	1732
GCTGGGTTTT GGTAAAAAA AAAAAAAAAA A	1763
•	
The sucrose phosphate - synthase has the following	
nucleotide sequence (Seq. ID No. 3):	
undisociae pedacuse (ped. 15 no. 2).	
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT	0044
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT Met Ala Gly Asn Asp	. 0044
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT	0044
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT  Met Ala Gly Asn Asp  5	
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT Met Ala Gly Asn Asp 5 TGG ATA AAC AGT TAT TTA GAG GCA ATT CTG GAT GTG GGT CCA	GGA 0089
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT  Met Ala Gly Asn Asp  5  TGG ATA AAC AGT TAT TTA GAG GCA ATT CTG GAT GTG GGT CCA  Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu Asp Val Gly Pro	GGA 0089 Gly
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT Met Ala Gly Asn Asp 5 TGG ATA AAC AGT TAT TTA GAG GCA ATT CTG GAT GTG GGT CCA	GGA 0089
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT  Met Ala Gly Asn Asp  5  TGG ATA AAC AGT TAT TTA GAG GCA ATT CTG GAT GTG GGT CCA  Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu Asp Val Gly Pro  10 15	GGA 0089 Gly 20
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT Met Ala Gly Asn Asp 5  TGG ATA AAC AGT TAT TTA GAG GCA ATT CTG GAT GTG GGT CCA Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu Asp Val Gly Pro 10 15  CTT GAT GAT GCA AAA TCA TCT TTG CTT TTG AGA GAA AGA GGC	GGA 0089 Gly 20 AGG 0134
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT  Met Ala Gly Asn Asp 5  TGG ATA AAC AGT TAT TTA GAG GCA ATT CTG GAT GTG GGT CCA  Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu Asp Val Gly Pro  10 15  CTT GAT GAT GCA AAA TCA TCT TTG CTT TTG AGA GAA AGA GGC  Leu Asp Asp Ala Lys Ser Ser Leu Leu Leu Arg Glu Arg Gly	GGA 0089 Gly 20 AGG 0134 Arg
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT Met Ala Gly Asn Asp 5  TGG ATA AAC AGT TAT TTA GAG GCA ATT CTG GAT GTG GGT CCA Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu Asp Val Gly Pro 10 15  CTT GAT GAT GCA AAA TCA TCT TTG CTT TTG AGA GAA AGA GGC	GGA 0089 Gly 20 AGG 0134
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT Met Ala Gly Asn Asp 5  TGG ATA AAC AGT TAT TTA GAG GCA ATT CTG GAT GTG GGT CCA Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu Asp Val Gly Pro 10 15  CTT GAT GAT GCA AAA TCA TCT TTG CTT TTG AGA GAA AGA GGC Leu Asp Asp Ala Lys Ser Ser Leu Leu Arg Glu Arg Gly 25 30	GGA 0089 Gly 20 AGG 0134 Arg 35
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT Met Ala Gly Asn Asp 5  TGG ATA AAC AGT TAT TTA GAG GCA ATT CTG GAT GTG GGT CCA Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu Asp Val Gly Pro 10 15  CTT GAT GAT GCA AAA TCA TCT TTG CTT TTG AGA GAA AGA GGC Leu Asp Asp Ala Lys Ser Ser Leu Leu Arg Glu Arg Gly 25 30  TTT AGT CCT ACT CGT TAC TTT GTT GAA GAA GTT ATC ACT GGT	GGA 0089 Gly 20 AGG 0134 Arg 35 TTT 0179
GGGCTGCAGG GAAGCTCTGA ACTTCAAAA ATG GCG GGA AAT GAT Met Ala Gly Asn Asp 5  TGG ATA AAC AGT TAT TTA GAG GCA ATT CTG GAT GTG GGT CCA Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu Asp Val Gly Pro 10 15  CTT GAT GAT GCA AAA TCA TCT TTG CTT TTG AGA GAA AGA GGC Leu Asp Asp Ala Lys Ser Ser Leu Leu Arg Glu Arg Gly 25 30	GGA 0089 Gly 20 AGG 0134 Arg 35 TTT 0179

GAT	GAA	ACC	GAC	CTT	CAT	CGT	TCA	TGG	GTT	CGG	GCA	CAA	GCA	ACA	0224
Asp	Glu	Thr	Asp	Leu	His	Arg	Ser	Trp	Val	Arg	Ala	Gln	Ala	Thr	
				55					60					65	
		CCT													0269
Arg	Ser	Pro	Gln	Glu	Arg	Asn	Thr	Arg	Leu	Glu	Asn	Met	Cys	Trp	
				70					75					80	
202	እመመ	TGG	חתת	TTTC:	CCT	CCT	CAG	እስር	λλC	CAC	CTTT	GNG	አአጥ	CAA	0314
		Trp													0314
Arg	TIE	πp	K211	85	VIG	Arg	GIII	כעם	90	GIII	Беи	GIU	ASII	95	
				0,5					30					,,,	
GAA	GCT	CAG	CGG	AAG	ACA	AAA	CGT	CGT	ATG	GAG	CTT	GAG	AGG	GGT	0359
Glu	Ala	Gln	Arg	Lys	Thr	Lys	Arg	Arg	Met	Glu	Leu	Glu	Arg	Gly	
				100					105		•			110	
		GAA													0404
Arg	Arg	Glu	Ala		Ala	Asp	Met	Ser		Asp	Leu	Ser			
				115					120					125	
GAA	AAG	GAC	ATT	TCA	GCT	CAT	GGT	GAT	AGC	ACC	CGT	CCT	AGA	TTG	0449
		Asp													
		•		130			-	-	135		_			140	
CCA	AGA	ATA	AAT	TCT	CTT	GAT	GCT	ATG	GAG	ACA	TGG	ATT	AGT	CAA	0494
Pro	Arg	Ile	Asn	Ser	Leu	Asp	Ala	Met	Glu	Thr	Trp	Ile	Ser	Gln	
				145					150				:	155	
				222	<b>C</b> TTC	m» ~	C.M.M.	cmm	መመረ	አመካ	a cm	C TTTT	C N m	CCE	0530
		GAA Glu													0539
GIN	rys	GIU	туз	160	TEA	TYL	nea		165	116	SEL	Den		170	
				100					-00				•	-,0	

TTG	ATA	CGA	GGT	GAA	AAC	ATG	GAA	CTT	GGC	CGT	GAT	TCT	GAT	ACT	0584
Leu	Ile	Arg	Gly	Glu	Asn	Met	Glụ	Leu	Gly	Arg	Asp	Ser	Asp	Thr	
				175					180					185	
GGT	GGT	CAG	GTT	AAG	TAT	GTG	GTT	GAG	CTT	GCA	AGG	GCT	CTA	GGT	0629
Gly	Gly	Gln	Val	Lys	Tyr	Val	Val	Glu	Leu	Ala	Arg	Ala	Leu	Gly	
-	_			190					195		-			200	
TCG	ATG	CCA	GGT	GTT	TAT	AGA	GTT	GAT	TTG	CTA	ACT	AGG	CAA	GTT	0674
Ser	Met	Pro	Gly	Val	Tyr	Arg	Val	Asp	Leu	Leu	Thr	Arq	Gln	Val	
			-	205	-			-	210			_		215	
TCA	тст	CCT	GAC	GTG	GAT	TGG	AGT	TAT	GGG	GAG	CCT	ACT	GAG	ATG	0719
					Asp										
				220	•				225					230	
CTG	AAT	CCA	AGG	GAT	TCC	AAT	GGT	TTT	GAT	GAT	GAT	GAT	GAT	GAA	0764
					Ser										
	••••		5	235			3		240	<b>L</b> -				245	
				•											
ATG	GGA	GAG	AGT	AGT	GGT	GCT	TAC	ATT	GTT	CGT	ATA	CCA	TTT	GGG	0809
					Gly										
	017	014	<b>D</b> 0.	250	1		-1-		255	5				260	
CCG	AGG	CDጥ	DAG	ጥፈጥ	ATC	GCA	AAA	GAA	GAG	СТТ	TGG	CCC	TAT	ATT	0854
					Ile										
LIO	ALG	wsh	בענה	265	T16	u	272		270	204				275	
				203					210					2,3	

CCT	GAA	TTT	GTT	GAT	GGT	GCT	CTA	AAC	CAC	ATA	GTT	CAA	ATG	TCC	0899
Pro	Glu	Phe	Val	Asp	Gly	Ala	Leu	Asn	His	Ile	Val	Gln	Met	Ser	
				280					285					290	
AAA	GTT	TTA	GGT	GAG	CAA	ATT	GGT.	AGC	GGG	GAA	ACA	GTT	TGG	CCA	0944
									Gly						
-2 -			-	295			_		300					305	
GTT	GCC	АТТ	CAT	GGA	CAT	TAT	GCT	GAT	GCT	GGT	GAT	TCT	GCT	GCT	0989
									Ala						
, ,			•••-	310		-1-			315		•			320	
				020											
ىلىلى	СТТ	тст	GGT	GGC	CTA	AAT	GTT	CCA	ATG	CTT	TTA	ACG	GGG	CAT	1034
									Met						
	204	001	1	325					330					335	
TCT	CTT	GGC	CGA	GAC	AAG	TTA	GAG	CAG	CTC	CTC	AAA	CAG	GGT	CGA	1079
									Leu						
		3		340	-				345		_			350	
ATG	тст	AAA	GAT	GAC	ATA	AAC	AAT	ACA	TAC	AAA	ATA	ATG	CGT	AGG	1124
									Tyr						
	•	<b>-</b> 2 -	•	355					360	-				365	
АТА	GAA	GCC	GAA	GAG	TTA	TCA	CTT	GAT	GCC	TCT	GAG	ATA	GTC	ATA	1169
									Ala						
11C	J_4			370		<del>-</del>			375					380	
				<b>J</b> , J					–						

ACT	AG'I	ACA	AGA	CAA	GAA	ATA	GAA	GAG	CAA	TGG	CAC	CTC	TAT	GAT	1214
Thr	Ser	Thr	Arg	Gln	Glu	Ile	Glu	Glu	Gln	Trp	His	Leu	Tyr	Asp	
				385					390					395	
GGG	TTT	GAT	CCT	GTG	CTA	GAA	CGT	AAA	CTC	CGT	GCT	AGG	ATG	AAG	1259
										Arg					
•		-		400				-	405	_				410	
CGT	GGT	GTA	AGC	TGT	TAT	GGA	AGG	TTC	ATG	ccc	CGG	ATG	GTT	GTT	1304
										Pro					
5	1			415	-1-	1	5		420		9			425	
ATT	CCT	CCT	GGA	ATG	GAA	TTC	AAT	CAT	ATT	GTT	CCA	CAT	GAG	GGT	1349
										Val					
			2	430					435					440	
				•••											
GAT	ATG	GAT	GGT	GAA	ACA	GAA	GAA	ACT	GAA	GAG	CAT	CCT	ACA	TCA	1394
asp	Met	Asp	Gly	Glu	Thr	Glu	Glu	Thr	Glu	Glu	His	Pro	Thr	Ser	
•		-	-	445					450					455	
CCT	GAT	CCA	CCT	ATC	TGG	GCT	GAG	ATT	ATG	CGC	TTC	TTT	TCT	AAA	1439
Pro	Asp	Pro	Pro	Ile	Trp	Ala	Glu	Ile	Met	Arg	Phe	Phe	Ser	Lys	
	•			460	-				465	,				- 470	
CCA	AGG	AAG	CCA	ATG	ATA	CTT	GCC	CTT	GCT	AGG	CCT	GAC	CCG	AAG	1484
										Arg					
	,	- 4		475					480	-		•		485	

MAI	ATC	ACG	ACT	TTG	GTC	AAA	GCA	TTT	GGA	GAA	TGC	CGT	CCA	1529
Asn	Ile	Thr	Thr	Leu	Val	Lys	Ala	Phe	Gly	Glu	Cys	Arg	Pro	
			490					495					500	
AGG	GAG	СТА	GCT	AAT	CTT	ACT	CTT	ATA	ATG	GGT	AAC	CGA	GAT	1574
,										-				
АТТ	GAC	GAG	ATG	TCA	AGC	ACC	AGT	TCT	TCA	GTT	CTC	CTG	TCA	1619
ርጥጥ	AAG	СТА	<u>አ</u> ጥጥ	GAT	CAA	TAC	GAC	СТТ	TAT	GGT	CAA	GTA	GCA	1664
Tea	ב עם	Dea			<b>U</b> 2	-1-			-,-	1				
			733					•						
CCC	מממ	תמס.	CAC	AAG	CAA	сст	САТ	<del>ር</del> ጥጥ	ССТ	GAG	ÄΤΤ	ТАТ	CGT	1709
	AAA													1709
	AAA Lys		His					Val				Tyr	Arg	1709
												Tyr		1709
			His					Val				Tyr	Arg	1709
Pro	Lys	His	His 550	Lys	Gln	Ala	Asp	Val 555	Pro	Glu	Ile	Tyr	Arg 600	
Pro GCA	Lys GCA	His AAG	His 550 ACA	Lys AAG	Gln GGA	Ala	Asp TTT	Val 555 ATT	Pro AAT	Glu CCA	Ile	Tyr TTT	Arg 600 ATT	1709 1754
Pro GCA	Lys	His AAG	His 550 ACA Thr	Lys AAG	Gln GGA	Ala	Asp TTT	Val 555 ATT Ile	Pro AAT	Glu CCA	Ile	Tyr TTT Phe	Arg 600 ATT Ile	
Pro GCA	Lys GCA	His AAG	His 550 ACA	Lys AAG	Gln GGA	Ala	Asp TTT	Val 555 ATT	Pro AAT	Glu CCA	Ile	Tyr TTT Phe	Arg 600 ATT	
Pro GCA	Lys GCA	His AAG	His 550 ACA Thr	Lys AAG	Gln GGA	Ala	Asp TTT	Val 555 ATT Ile	Pro AAT	Glu CCA	Ile	Tyr TTT Phe	Arg 600 ATT Ile	
Pro GCA Ala	Lys GCA Ala	His AAG Lys	His 550 ACA Thr 605	Lys AAG Lys	Gln GGA Gly	Ala GTC Val	Asp TTT Phe	Val 555 ATT Ile 610	Pro AAT Asn	Glu CCA Pro	Ile GCT Ala	Tyr TTT Phe	Arg 600 ATT Ile 615	1754
Pro GCA Ala	Lys GCA Ala TTT	AAG Lys GGG	His 550 ACA Thr 605	Lys AAG Lys ACT	Gln GGA Gly	Ala GTC Val	TTT Phe	Val 555 ATT Ile 610	Pro AAT Asn	Glu CCA Pro	GCT Ala	TYT TTT Phe GGT	Arg 600 ATT Ile 615	
Pro GCA Ala	Lys GCA Ala	AAG Lys GGG	His 550 ACA Thr 605 CTG Leu	Lys AAG Lys ACT	Gln GGA Gly	Ala GTC Val	TTT Phe	Val 555 ATT Ile 610 GCA Ala	Pro AAT Asn	Glu CCA Pro	GCT Ala	TYT TTT Phe GGT Gly	Arg 600 ATT Ile 615 TTA Leu	1754
Pro GCA Ala	Lys GCA Ala TTT	AAG Lys GGG	His 550 ACA Thr 605	Lys AAG Lys ACT	Gln GGA Gly	Ala GTC Val	TTT Phe	Val 555 ATT Ile 610	Pro AAT Asn	Glu CCA Pro	GCT Ala	TYT TTT Phe GGT Gly	Arg 600 ATT Ile 615	1754
	AGG Arg ATT Ile	AGG GAG Arg Glu ATT GAC Ile Asp	AGG GAG CTA Arg Glu Leu  ATT GAC GAG Ile Asp Glu  CTT AAG CTA	AGG GAG CTA GCT Arg Glu Leu Ala 505  ATT GAC GAG ATG Ile Asp Glu Met 520  CTT AAG CTA ATT	AGG GAG CTA GCT AAT Arg Glu Leu Ala Asn 505  ATT GAC GAG ATG TCA Ile Asp Glu Met Ser 520  CTT AAG CTA ATT GAT Leu Lys Leu Ile Asp	AGG GAG CTA GCT AAT CTT Arg Glu Leu Ala Asn Leu 505  ATT GAC GAG ATG TCA AGC Ile Asp Glu Met Ser Ser 520  CTT AAG CTA ATT GAT CAA Leu Lys Leu Ile Asp Gln	AGG GAG CTA GCT AAT CTT ACT Arg Glu Leu Ala Asn Leu Thr 505  ATT GAC GAG ATG TCA AGC ACC Ile Asp Glu Met Ser Ser Thr 520  CTT AAG CTA ATT GAT CAA TAC Leu Lys Leu Ile Asp Gln Tyr	AGG GAG CTA GCT AAT CTT ACT CTT Arg Glu Leu Ala Asn Leu Thr Leu 505  ATT GAC GAG ATG TCA AGC ACC AGT Ile Asp Glu Met Ser Ser Thr Ser 520  CTT AAG CTA ATT GAT CAA TAC GAC Leu Lys Leu Ile Asp Gln Tyr Asp	AGG GAG CTA GCT AAT CTT ACT CTT ATA Arg Glu Leu Ala Asn Leu Thr Leu Ile 505 TCA AGC ACC AGT TCT Ile Asp Glu Met Ser Ser Thr Ser Ser 520 CTT AAG CTA ATT GAT CAA TAC GAC CTT Leu Lys Leu Ile Asp Gln Tyr Asp Leu	AGG GAG CTA GCT AAT CTT ACT CTT ATA ATG ATG GAC GAC CTA SOS SOS SOS SOS SOS SOS SOS SOS SOS SO	AGG GAG CTA GCT AAT CTT ACT CTT ATA ATG GGT ATT GAC GAC CTT TAT GGT AAG Lys Leu Lys Leu Ile Asp Glu Att Ser Sch Tac Sch Ser Sch	AGG GAG CTA GCT AAT CTT ACT CTT ATA ATG GGT AAC ATG GAT SOON SOON SOON SOON SOON SOON SOON SOO	AGG GAG CTA GCT AAT CTT ACT CTT ATA ATG GGT AAC CGA Arg Glu Leu Ala Asn Leu Thr Leu Ile Met Gly Asn Arg 505 ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' '	AGG GAG CTA GCT AAT CTT ACT CTT ATA ATG GGT AAC CGA GAT ATG GAC GAG GAT ACT GAC GAG GAT ACT GAC GAG GAG ATG GAC GAG ATG GAC GAG ATG GAC AGC AGT TCT TCA GTT CTC CTG TCA GAC ACC AGT TCT AAG CTA ATT GAT GAT CAA TAC GAC CTT TAT GGT CAA GTA GCA Leu Lys Leu Ile Asp Gln Tyr Asp Leu Tyr Gly Gln Val Ala

CCG	ATG	GTT	GCT	ACG	AAA	AAT	GGA	GGC	CCT	GTT	GAT	ATC	CAG	AGG	1844
Pro	Met	Val	Ala	Thr	Lys	Asn	Gly	Gly	Pro	Val	Asp	Ile	Gln	Arg	
				635					640					645	
GTC	CTT	GAT	ААТ	GGT	CTT	CTT	GTG	GAT	CCT	CAT	GAG	CAG	CAG	TCT	1889
Val	Leu	Asp	Asn	Gly	Leu	Leu	Val	Asp	Pro	His	Glu	Gln	Gln	Ser	
				650					655					660	
ATT	GCT	ACT	GCT	TTG	CTG	AAG	CTT	GTT	GCT	GAT	AAG	CAA	СТА	TGG	1934
Ile	Ala	Thr	Ala	Leu	Leu	Lys	Leu	Val	Ala	Asp	Lys	Gln	Leu	Trp	
				665		•			670		_,			675	
ACA	AAA	TGC	CAG	CAA	AAT	GGA	CTG	AAA	AAT	ATT	CAT	CTC	TAC	TCT	1979
											His				
		•		680		•		•	685				_	690	
TGG	CCA	GAG	CAT	TCG	AAG	ACA	TAC	CTA	TCT	CGA	ATA	GCC.	AGT	TCG	2024
											Ile				
•				695	-		-		700	•				705	
AGA	CAA	AGG	CAA	CCA	CAG	TGG	CAA	AGA	AGT	AGT	GAT	GAA	GGG	CTT	2069
											Asp				
,		,		710		-		_	715		-		_	720	
									•						
GAC	AAT	CAA	GAG	CCT	GAA	TCT	CCA	AGT	GAT	TCT	TTA	AGA	GAT	ATA	2114
											Leu				
- 1				725					730			_		735	

AAG	GAT	ATA	TCT	CTA	AAC	CTT	GAA	GTT	CTC	GTT	AGA	CCG	GAG	AAA	2159
Lys	Asp	Ile	Ser	Leu	Asn	Leu	Glu	Val	Leu	Val	Arg	Pro	Glu	Lys	
				740					745					750	
AGG	GTG	AAG	ACG	TTG	AAA	ATC	TTG	·GGA	TTG	ATG	ACA	AAA	GCA	TAA	2204
Arg	Val	Lys	Thr	Leu	Lys	Ile	Leu	Gly	Leu	Met	Thr	Lys	Ala	Asn	
				755					760					765	
TCG	AGA	ATG	CTG	TTA	TGT	TCA	TGG	TCT	AAT	GGT	GTC	CAT	AAG	ATG	2249
Ser	Arg	Met	Leu	Leu	Cys	Ser	Trp	Ser	Asn	Gly	Val	His	Lys	Met	
				770					775					780	
CTT	CGG	AAG	GCT	CGG	TTC	TCT	GAC	AAA	GTA	GAT	CAG	GCT	TCT	AGT	2294
Leu	Arg	Lys	Ala	-	Phe	Ser	Asp	Lys	Val	Asp	Gin	Aic	Ser	Ser	
				785					790					795	
			GCA								•				2339
Lys	Tyr	Pro	Ala	Phe	Arg	Arg	Arg	Lys	Leu	Ile	Tyr	Val	Ile	Ala	
				800					805					810	
										<i>-</i>					
			GAT												2384
Val	Asp	Gly	Asp		Glu	Asp	Gly	Leu		Asp	Ile	Val			
				815					820				:	825	
											•				
			GCT												2429
Ile	Phe	Asp	Ala	Ala	Gly	Lys	Glu	Lys	Ile	Glu	Gly	Ser	Ile	Gly	

TTT	ATA	TTG	TCA	ACA	TCC	TAT	TCT	ATG	CCC	GAA	ATT	CAG	AAC	TAT	2474
Phe	Ile	Leu	Ser	Thr	Ser	Tyr	Ser	Met	Pro	Glu	Ile	Gln	Asn	Tyr	
				845					850					855	
TTG	CTA	TCA	AAA	GGC	TTC	AAT	CTT	CAT	GAT	TTT	GAT	GCA	TAT	ATA	2519
Leu	Leu	Ser	Lys	Gly	Phe	Asn	Leu	His	Asp	Phe	Asp	Ala	Tyr	Ile	
				860					865					870	
TGC	AAC	AGT	GGG	AGT	GAG	TTG	TAC	TAT	TCA	TCT	TTG	AAC	TCA	GAG	2564
Cys	Asn	Ser	Gly	Ser	Glu	Leu	Tyr	Tyr	Ser	Ser	Leu	Asn	Ser	Glu	
				875					880					885	
GAG	AGT	AAT	ATT	ATA	GCA	GAT	TCA	GAT	TAC	CAT	TCA	CAC	ATA	GAG	2609
Glu	Ser	Asn	Ile	Ile	Ala	Asp	Ser	Asp	Tyr	His	Ser	His	Ile	Glu	
				890					895				!	900	
TAC	AGA	TGG	GGT	GGA	GAA	GGC	CTT	AGA	AGG	ACT	TTG	CTT	CGC	TGG	2654
				GGA Gly											2654
													Arg		2654
				Gly					Arg				Arg	Trp	2654
Tyr	Arg	Trp	Gly	Gly 905	Glu	Gly	Leu	'Arg	Arg 910	Thr	Leu	Leu	Arg	Trp 915	2654
Tyr GCA	Arg	Trp	Gly ATC	Gly 905 ACA	Glu GAA	Gly AAA	Leu AAT	'Arg	Arg 910 GAA	Thr	Leu GAA	Leu GAA	Arg CAG	Trp 915 GTT	2654
Tyr GCA	Arg	Trp	Gly ATC	Gly 905	Glu GAA	Gly AAA	Leu AAT	'Arg	Arg 910 GAA	Thr	Leu GAA	Leu GAA	Arg CAG	Trp 915 GTT	
Tyr GCA	Arg	Trp	Gly ATC	Gly 905 ACA	Glu GAA	Gly AAA	Leu AAT	'Arg	Arg 910 GAA	Thr	Leu GAA	Leu GAA	Arg CAG Gln	Trp 915 GTT	
Tyr GCA	Arg	Trp	Gly ATC	Gly 905 ACA Thr	Glu GAA	Gly AAA	Leu AAT	'Arg	Arg 910 GAA Glu	Thr	Leu GAA	Leu GAA	Arg CAG Gln	Trp 915 GTT Val	
Tyr GCA Ala	Arg GCT Ala	Trp TCC Ser	Gly ATC Ile	Gly 905 ACA Thr 920	Glu GAA Glu	Gly AAA Lys	Leu AAT Asn	GGT Gly	Arg 910 GAA Glu 925	Thr AAC Asn	Leu GAA Glu	Leu GAA Glu	Arg CAG Gln	Trp 915 GTT Val 930	2699
Tyr GCA Ala	Arg GCT Ala	TCC Ser	Gly ATC Ile	Gly 905 ACA Thr 920	GAA Glu GAA	Gly AAA Lys GTT	Leu AAT Asn	GGT Gly	Arg 910 GAA Glu 925	Thr AAC Asn	Leu GAA Glu TGC	Leu GAA Glu TTT	CAG Gln GCG	Trp 915 GTT Val 930	
Tyr GCA Ala	Arg GCT Ala	TCC Ser	Gly ATC Ile	Gly 905 ACA Thr 920 GAA Glu	GAA Glu GAA	Gly AAA Lys GTT	Leu AAT Asn	GGT Gly	Arg 910 GAA Glu 925 GGT Gly	Thr AAC Asn	Leu GAA Glu TGC	Leu GAA Glu TTT	CAG Gln GCG Ala	Trp 915 GTT Val 930 TTT Phe	2699
Tyr GCA Ala	Arg GCT Ala	TCC Ser	Gly ATC Ile	Gly 905 ACA Thr 920	GAA Glu GAA	Gly AAA Lys GTT	Leu AAT Asn	GGT Gly	Arg 910 GAA Glu 925	Thr AAC Asn	Leu GAA Glu TGC	Leu GAA Glu TTT	CAG Gln GCG Ala	Trp 915 GTT Val 930	2699

AAA	ATA	AAG	AAC	CAA	AAT	AAG	GTT	CCC	CCT	ACG	AAG	GAG	CTC	CGC	2789
Lys	Ile	Lys	Asn	Gln	Asn	Lys	Val	Pro	Pro	Thr	Lys	Glu	Leu	Arg	
				950					955					960	
AAG	TCA	ATG	AGG	ATT	CAA	GCT	CTT	CGT	TGC	CAT	GTG	ATT	TAC	TGT	2834
Lys	Ser	Met	Arg	Ile	Gln	Ala	Leu	Arg	Cys	His	Val	Ile	Tyr	Cys	
				965					970					975	
CAG	AAC	GGA	TCT	AAA	ATG	AAT	GTG	ATT	CCA	GTA	CTA	GCA	TCC	CGT	2879
Gln	Asn	Gly	Ser	Lys	Met	Asn	Val	Ile	Pro	Val	Leu	Ala	Ser	Arg	
		-		980					985					990	
TCT	CAA	GCC	CTC	AGG	TAT	CTT	TAT	GTT	CGT	TGG	GGA	GTT	GAG	TTG	2924
	Gln														
				995	_				.000		_			005	
TCG	ÀAG	ATG	GTT	GTC	TTT	GTT	GGA	GAA	TGT	GGT	GAC	ACA	GAT	TAT	2969
	Lys														
	<u>,,</u>			010			_		015	_	_			020	
GAA	GGC	TTG	СТТ	GGC	GGG	GTC	CAT	AAA	ACC	GTA	ATA	CTG	AAG	GGA	3014
	Gly														
	1			1025	•				030					035	
•															
ርጥር	TCC	AAC	ACT	GCT	TTA	AGG	TCT	CTC	CAT	GCC	AAC	AGA	AGT	TAC	3059
	Ser														
· u.ı	UCL			040		· 5			045			3		050	
			_												

CTT	TCA	$\mathtt{CAT}$	GTC	GTG	TCG	CTT	GAC	AGC	CCC	AAT	ATT	GGC	GAG	3104
Leu	Ser	His	Val	Val	Ser	Leu	Asp	Ser	Pro	Asn	Ile	Gly	Glu	
		1	1055				1	.060				1	065	
AGC	AAA	GGG	TGC	AGC	AGC	TCC	GAG	ATC	CAG	TCC	ATC	GTC	ACA	3149
Ser	Lys	Gly	Cys	Ser	Ser	Ser	Glu	Ile	Gln	Ser	Ile	Val	Thr	
		1	1070				1	075				1	080	
													•	
CTC	TCC	AAA	GCT	TAA	TCAG	ATAT	CT C	CTG	CTTTC	т т	TGG	GTAAC	3	3197
									•					
GTTT	'CA 'I	CTT	TATO	A TI	LATAT	CATA	AGA	TACI	ATA	TAAC	CAC	CTT		3247
GTAA	GT C	AGTO	CCAT	'A A'	ATAAT	ATGI	' ACI	TCAC	GAAC	CACA	ATA	CTT		3297
STTG	GT I	CAGI	TAGTO	A TI	TAGTO	TCAT	LAA '	TAAT	CATA	TAAT	TAC	ACA		3347
CTGI	TA A	CTAC	TGGI	'A A'	CATCI	TAAGO	TCA	ACA	AATA	AGAT	GTA	AAA		3397
AGTA	TG C	CAAA	rgaat	T GO	TAGO	TGTI	GAT	CTCI	TTTC	CCTT	TAT	гст		3447
rati	TC I	TTC	CTCAT	C TO	CATGI	AAA?	ACA	\ATTI	TOT	GAAC	GTG	CAC		3497
rtti	cc c	CTTA	TATA	AT CT	rgtai	TATT	TCI	ract?	TTT	TTTC	TTTC	GTA		3547
<b></b>														
<b>~ &gt; </b> ~ <i>C</i>										cmm.				3597
ľATU	CT U	CACT	CGAC	G A	PIGAL	LAAT	. AAA	YTAAC	CCGG	CTT	CTA	JAT.		3391
rarc	Cr C	CTCAT	rcgac	G A	·	LAAT.	: AAA	ATAAC	CCGG	CTTC	3CTA	AAT.		3397
	AGC GET GTTT GTAA GTAGTA	AGC AAA Ser Lys CTC TCC Leu Ser CTTTCA T CTTTCA T CTTTTCA T	AGC AAA GGG Ser Lys Gly CTC TCC AAA Leu Ser Lys CTTTCA TCTTA CTAAGT CAGTO CTGTTA ACTAC	Leu Ser His Val  1055  AGC AAA GGG TGC Ser Lys Gly Cys 1070  CTC TCC AAA GCT Leu Ser Lys Ala 1085  CTTTCA TCTTATATO  CTAAGT CAGTCCCAT  CTGTTA ACTAGTGGT  AGTATG GAAATGAAT  CATTTC TTTCCTCAT	Leu Ser His Val Val  1055  AGC AAA GGG TGC AGC Ser Lys Gly Cys Ser  1070  CTC TCC AAA GCT TAA Leu Ser Lys Ala End 1085  CTTTCA TCTTATATGA TT  CTAAGT CAGTCCCATA AT  CTGTTA ACTAGTGGTA AT  AGTATG GAAATGAATT GC  CTTTCC CCTTATATAT CT	Leu Ser His Val Val Ser  1055  AGC AAA GGG TGC AGC AGC Ser Lys Gly Cys Ser Ser 1070  CTC TCC AAA GCT TAA TCAC Leu Ser Lys Ala End 1085  CTTTCA TCTTATATGA TTATAT  CTAAGT CAGTCCCATA ATAATA  CTGTTA ACTAGTGGTA ATAATA  AGTATG GAAATGAATT GCTAGC  CATTTCC TCTCATC TCATGT  CTTTCC CCTTATATAT CTGTAT	Leu Ser His Val Val Ser Leu  1055  AGC AAA GGG TGC AGC AGC TCC Ser Lys Gly Cys Ser Ser Ser 1070  CTC TCC AAA GCT TAA TCAGATAT Leu Ser Lys Ala End 1085  GTTTCA TCTTATATGA TTATATCATA GTAAGT CAGTCCCATA ATAATAATGT CTGTTA ACTAGTGGTA ATATCTAAGC AGTATG GAAATGAATT GCTAGCTGTT CATTTCC TCTCCATC TCATGTAAAA	Leu Ser His Val Val Ser Leu Asp  1055  AGC AAA GGG TGC AGC AGC TCC GAG Ser Lys Gly Cys Ser Ser Ser Glu  1070  CTC TCC AAA GCT TAA TCAGATATCT C Leu Ser Lys Ala End  1085  CTTTCA TCTTATATGA TTATATCATA AGA  CTAAGT CAGTCCCATA ATAATAATGT ACC  CTGTTA ACTAGTGGTA TTAGTCTCAT AAT  CTGTTA ACTAGTGGTA ATATCTAAGC TCA  AGTATG GAAATGAATT GCTAGCTGTT GAT  CATTTCC TTTCCTCATC TCATGTAAAA ACA  CTTTTCC CCTTATATAT CTGTATTATT TCT	Leu Ser His Val Val Ser Leu Asp Ser  1055 1060  AGC AAA GGG TGC AGC AGC TCC GAG ATC Ser Lys Gly Cys Ser Ser Ser Glu Ile  1070 1075  CTC TCC AAA GCT TAA TCAGATATCT GCTGC Leu Ser Lys Ala End  1085  CTATCA TCTTATATGA TTATATCATA AGATACT  CTAGT CAGTCCCATA ATAATAATGT ACTTCAC  CTGTTA ACTAGTGA TTAGTCTCAT AATAATC  CTGTTA ACTAGTGGTA ATATCTAAGC TCAACAA  AGTATG GAAATGAATT GCTAGCTGTT GATCTC  CTATTC TTTCCTCATC TCATGTAAAA ACAATTC  CTTTTCC CCTTATATAT CTGTATTATT TCTACTA	Leu Ser His Val Val Ser Leu Asp Ser Pro  1055 1060  AGC AAA GGG TGC AGC AGC TCC GAG ATC CAG Ser Lys Gly Cys Ser Ser Ser Glu Ile Gln  1070 1075  CTC TCC AAA GCT TAA TCAGATATCT GCTGCTTTC Leu Ser Lys Ala End  1085  CTTTCA TCTTATATGA TTATATCATA AGATACTATA  CTAAGT CAGTCCCATA ATAATAATGT ACTTCAGAAC  CTTGTTA ACTAGTGGTA ATATCTAAGC TCAACAATAA  AGTATG GAAATGAATT GCTAGCTGTT GATCTCTTC  CTTTCC CCTTATATAT CTGTATTATT TCTACTATTT	Leu Ser His Val Val Ser Leu Asp Ser Pro Asn 1055 1060  AGC AAA GGG TGC AGC AGC TCC GAG ATC CAG TCC Ger Lys Gly Cys Ser Ser Ser Glu Ile Gln Ser 1070 1075  CTC TCC AAA GCT TAA TCAGATATCT GCTGCTTTCT TT Leu Ser Lys Ala End 1085  CTTTCA TCTTATATGA TTATATCATA AGATACTATA TAAC CTAAGT CAGTCCCATA ATAATAATGT ACTTCAGAAC CACA CTTGGT TCAGTAGTGA TTAGTCTCAT AATAATCATA TAAT CTGTTA ACTAGTGGTA ATATCTAAGC TCAACAATAA AGAT AGTATG GAAATGAATT GCTAGCTGTT GATCTCTTTC CCTT CTTTCC CCTTATATAT CTGTATTATT TCTACTATTT TTTC	Leu Ser His Val Val Ser Leu Asp Ser Pro Asn Ile  1055 1060  AGC AAA GGG TGC AGC AGC TCC GAG ATC CAG TCC ATC Ser Lys Gly Cys Ser Ser Ser Glu Ile Gln Ser Ile  1070 1075  CTC TCC AAA GCT TAA TCAGATATCT GCTGCTTTCT TTTGGG Leu Ser Lys Ala End  1085  CTTTCA TCTTATATGA TTATATCATA AGATACTATA TAAGCACG CTAAGT CAGTCCCATA ATAATAATGT ACTTCAGAAC CACAATAG CTTGGT TCAGTAGTGA TTAGTCTCAT AATAATCATA TAATTACA CTGTTA ACTAGTGGTA ATATCAAGC TCAACAATAA AGATGTAA AGTATG GAAATGAATT GCTAGCTGTT GATCTCTTTC CCTTTATA CTATTTC TTTCCTCATC TCATGTAAAA ACAATTTTCT GAAGGTGT	Leu Ser His Val Val Ser Leu Asp Ser Pro Asn Ile Gly 1055 1060 1  AGC AAA GGG TGC AGC AGC TCC GAG ATC CAG TCC ATC GTC Ser Lys Gly Cys Ser Ser Ser Glu Ile Gln Ser Ile Val 1070 1075 1  CTC TCC AAA GCT TAA TCAGATATCT GCTGCTTTCT TTTGGGTAAC Leu Ser Lys Ala End	AGC AAA GGG TGC AGC AGC TCC GAG ATC CAG TCC ATC GTC ACA SET Lys Gly Cys Ser Ser Ser Glu Ile Gln Ser Ile Val Thr 1070 1075 1080  CTC TCC AAA GCT TAA TCAGATATCT GCTGCTTTCT TTTGGGTAAG  Leu Ser Lys Ala End 1085  CTTTCA TCTTATATGA TTATATCATA AGATACTATA TAAGCACCTT  CTAAGT CAGTCCCATA ATAATAATGT ACTTCAGAAC CACAATACTT  CTTGGT TCAGTAGTGA TTAGTCTCAT AATAATCATA TAATTACACA  CTGTTA ACTAGTGGTA ATATCTAAGC TCAACAATAA AGATGTAAAA  AGTATG GAAATGAATT GCTAGCTGTT GATCTCTTTC CCTTTATTCT  CTTTCC CCTTATATAT CTGTATTATT TCTACTATTT TTTGTTTGTA

The sucrose-synthase has the following nucleotide sequence (Seq. ID No. 4):

CT	GCA	GGA	GGG	AAA	CAA	ATT	CTT	AGC	GAT	GGC	CCG	TTT	AGC	GAA	0044
	Ala	Gly	Gly	Lys	Gln	Ile	Leu	Ser	Asp	Gly	Pro	Phe	Ser	Glu	
					5			•		10					
			TCT												0089
	Leu	Arg	Ser	Ala		Glu	Ala	Ile	Val		Pro	Pro	Phe	Val	
15					20					25			·		
GCT	ልጥል	GCA	GTC	CGT	CCA	AGA	CCT	GGA	GTT	TGG	GAA	TAT	GTT	CGT	0134
			Val												
30					35	•		-		40		-		· ·	
GTT	AAT	GTC	TCT	GAA	CTG	AAT	GTG	GAG	CAG	CTA	ACT	GTG	TCT	GAG	0179
Val	Acn	۷al	Ser	Glu	Leu	Asn	Val	Glu	Glrı	Leu	Thr	Val	Ser	Glu	
45					50					55					
			TTC												0224
_	Leu	HIS	Phe	гÀг	65 65	GIU	Leu	vai	Asp	70	гàг	Ala	Asp	ASP	
60					65					70					
CAC	TAT	GTG	CTT	GAG	CTT	GAT	TTC	GAG	CCT	TTT	AAT	GAA	TCA	GTT	0269
His	Tyr	Val	Leu	Glu	Leu	Asp	Phe	Glu	Pro	Phe	Asn	Glu	Ser	Val	
75					80					85					
			ACT												0314
Pro	Arg	Pro	Thr	Arg	Ser	Ser	Ser	Ile	Gly	Asn	Gly	Val	Gln	Phe	
90					95					100					
ርፐር	ከ ልጥ	CGG	CAC	CTG	TCA	TCA	AGC	ATG	TTC	TGC	AAC	AAA	GAT	TGC	0359
			His												
105		3			110					115		_		-	

TTG	GAG	CCG	TTA	CTT	GAT	TTT	CTT	AGA	GTG	CAC	AAA	CAT	AAA	GGA	0404
Leu	Glu	Pro	Leu	Leu	Asp	Phe	Leu	Arg	Val	His	Lys	His	Lys	Gly	
120					125					130					
"										ACT					0449
Val	Val	Met	Met	Leu		Asp	Arg	Ile	Gln	Thr	Ile	Gln	Arg	Leu	
135					140					145					
CAC	mcm	CCA	mm.c	T C T	**	CCT	CAC	CAT	ሙአሙ	CTT	N TO C	222	CTTT.	CCA	0494
										Leu					0494
150	261	VIG	Deu	Der	155	niu	GIU	nap	TYL	160	116	Dys	Dea	rio	
150					100					100					
GCA	GAT	ACA	ССТ	TAC	TCT	GAG	TTC	GAA	TTT	GTA	ATC	CAA	GGT	ATG	0539
Ala	Asp	Thr	Pro	Tyr	Ser	Glu	Phe	Glu	Phe	val	lie	G) n	Gly	Met	
165					170					175					
GGT	TTT	GAA	AGA	GGC	TGG	GGT	GAT	ACT	GCT	GAA	AGG	GTT	CTA	GAA	0584
Gly	Phe	Glu	Arg	Gly	Trp	Gly	Asp	Thr	Ala	Glu	Arg	Val	Leu	Glu	
180					185					190					
	1 mc	G 3 m	OM N	C/III N	Cm 3	C N III	»mc	CIIII	C2 C	GCT	000	C N M	000	mem	0620
										Ala					0629
195	Mec	nis	теп	Dea	200	ASP	116	Leu		205	FLO	rsb	PIO	Ser	
193					200					205					
ACA	TTA	GAG	ACA	TTT	CTG	GGA	AGA	СТТ	CCC	ATG	GTG	TTT	AAT	GTG	0674
Thr	Leu	Glu	Thr	Phe	Leu	Gly	Arg	Leu	Pro	Met	Val	Phe	Asn	Val	
210					215					220					

GTC	ATT	TTG	TCT	GTA	CAT	GGA	TAT	TTT	GGA	CAG	GCA	CAT	GTG	CTC	0719
Val	Ile	Leu	Ser	Val	His	Gly	Tyr	Phe	Gly	Gln	Ala	His	Val	Leu	
225					230					235					
_					GGT										0764
Gly	Leu	Pro	Asp	Thr	Gly	Gly	Gln	Ile	Val	Tyr	Ile	Leu	Asp	Gln	
240					245					250					
														CAA	0809
Val	Arg	Ser	Leu	Glu	His	Glu	Met	Leu	Gln		Ile	Lys	Lys	Gln	
255					260					265					
					CCT										0854
_	Leu	Asp	Val	Thr	Pro	Arg	IIe	Leu	Ile		Ser	Arg	Leu	TIE	
270					275					280					
00m	C 2 C	COM	***	CCC	ACC	A CG:	ጥርር	יית מּיַּת	C 2: A	CGT	ልጥር	GAG	מממ	GTC.	0899
					Thr										0055
	ASP	Ald	rys	Giy	290	****	Cys	ASII		295		014	2,5	<b>V</b> 41	
285					250					2,5					
ልርጥ	GGA	ACA	GAG	CAT	GCT	AGT	ATC	CTG	AGA	GTT	CCT	TTC	CGA	TCA	0944
					Ala										
300	Cry	****			305					310			•		
GAG	AAA	GGA	ATC	СТС	CGC	AAA	TGG	ATA	TCT	AGA	TTT	GAT	GTA	TGG	0989
					Arg										
315	-	-			320					325					

CCT	TAT	TTA	GAG	ACC	TTC	ACT	GAG	GAT	GCA	GCT	GGT	GAA	ATT	ATT	1034
Pro	Tyr	Leu	Glu	Thr	Phe	Thr	Glu	Asp	Ala	Ala	Gly	Glu	Ile	Ile	
330					335					340					
GGC	GAG	TTG	CAG	GGT	CGT	CCA	GAT	·CTG	ATA	ATT	GGC	AAC	TAC	AGC	1079
Gly	Glu	Leu	Gln	Gly	Arg	Pro	Asp	Leu	Ile	Ile	Gly	Asn	Tyr	Ser	
345					350					355					
GAT	GGG	AAT	ATA	GTT	GCT	TCT	TTA	TTG	TCC	CAC	AAA	ATG	GGT	GTC	1124
Asp	Gly	Asn	Ile	Val	Ala	Ser	Leu	Leu	Ser	His	Lys	Met	Gly	Val	
360					365					370					
										AAA					1169
Thr	Gln	Cys	Asn	Ile	Ala	His	Ala	Leu	Glu	Lys	Thr	Lys	tyr	Pro	
375					380					385					
										GAC					1214
-	Ser	Asp	Ile	Tyr	_	Lys	Arg	Phe	Glu	Asp	Lys	Tyr	His	Phe	
390					395					400					
	<b></b>	<b>~</b>	mmm	<b>50.</b>	a am	<b>63.6</b>	mmc	3 mc	663	3.000		0 h m	C C C	63.E	****
										ATG					1259
	Cys	GIN	Pne			Asp	Leu	met		Met	ASN	nis	Ala	Asp	
405					410					415					
mmc	አመሮ	א תיתי	N C C	λcm	እ ርጥ	ישאר	CDD	GAG	מיתה	GCT	GG A	ACG	AAG	ል ልጥ	1304
										Ala					1304
420	TTE	116	TITE	261	425	TYL	3111	JIU		430	GIY	1111	בעב	non	
720					423					450				•	

ACT	GTT	GGT	CAA	TAT	GAA	AGC	CAT	AAG	GCC	TTT	ACT	TTT	CCG	GGG	1349
Thr	Val	Gly	Gln	Tyr	Glu	Ser	His	Lys	Ala	Phe	Thr	Phe	Pro	Gly	
435					440					445					
			GTG												1394
Leu	Tyr	Arg	Val	Val	His	Gly	Ile	Asp	Val	Phe	Asp	Pro	Lys	Phe	
450					455					460					
			TCG												1439.
Asn	Ile	Val	Ser	Pro		Ala	Asp	Met	Ala		Tyr	Phe	Pro	Phe	
465					470					475					
			-					3.00	max	cmm.	03 m	202	CTTTT	አጥአ	1484
			GAT												1404
	Glu	Lys	Asp	Val		Cys	Ter	Thr	ser	190	nis	Arg	Pen	116	
480					485					490					
					• •										
63.6	C	CMC	CTI N	መጥር	מממ	CCT	GAG	CAG	AAC	GAA	GAA	CAC	ATT	GGT	1529
			Leu												
	GIII	пеп	Dea	1110	500		.020	·		505				•	
495					500										
сπа	ጥጥል	GAT	GAT	ACC	TCA	AAG	CCA	ATT	ATA	TTT	TCC	ATG	GCG	AGG	1574
			Asp												
510	БСи	p			515	•				520					
210															
СТА	GAC	CGT	GTG	AAG	TAA	ATA	ACA	GGG	CTG	GTA	GAG	TGC	TAT	GGC	1619
			Val												
525		- 2		-	530					535					

AAG	AAT	GCG	AAA	CTC	. AGG	GAA	CTG	GCA	AAC	CTG	GTT	GTA	GTG	GCT	166
Lys	Asn	Ala	Lys	Leu	Arg	Glu	Leu	Ala	Asn	Leu	Val	Val	Val	Ala	
540					545					550					
GGG	TAC	AAT	GAT	GTA	AAA	AAG	TCG	AAT	GAC	AGG	GAG	GAA	АТТ	GCC	1709
										Arg					
555	-		•		560	•				565					
GAA	ATC	GAG	AAG	ATG	CAC	AGG	CTT	ATA	CAG	GAG	TAT	AAT	TTA	AGA	1754
										Glu					
570			•		575	_				580				5	
GGA	CAA	TTT	CGC	TGG	ATT	GCT	TCT	CAA	ACA	AAT	AGA	GTA	CGA	AAT	1799
										Asn					
- 585				-	590					595	, ,		,		
GGT	GAA	CTC	TAT	CGC	TAC	ATT	TGT	GAC	AAA	GGA	GGT	ATT	TTT	GCG '	1844
										Gly					
600			-		605		-	-	_	610	•				
CAG	CCT	GCA	TTT	TAT	GAA	GCA	TTT	GGG	CTT	ACA	GTT	GTT	GAA	GCC	1889
										Thr					
615				-	620			•		625					
						•									
ATG	ACC	TGT	GGT	CTT	ccc	ACA	TTT	GCT	ACC	TGC	CAC	GGT	GGT	CCA	1934
										Cys					
630		-	•		635					640		•	<b>-</b> .		

			ATA Ile											CCA Pro	1979
645					650					655					
														AAG	2024
•	His	Ala	Asp	Gln		Glu	Lys	Met	Thr	Glu 670	Phe	Phe	Val	Lys	
660					665					670					
															2262
			GAT Asp												2069
675	Arg	GIU	Asp	PIO	680	ıyı	пр	1111	пур	685	261	VIG	Gly	Gly	
0,0															
ጥጥል	СТА	AGG	ATC	ΔΔΔ	GAA	AGA	тат	ACC	TGG	CAA	AAG	тат	тст	GAA	2114
			Ile												
690		_			695		•	•		700					
AGG	TTA	ATG	ACA	TTG	GCA	GGG	GTG	TAT	GGT	TTC	TGG	AAA	TAT	GTC	2159
Arg	Leu	Met	Thr	Leu	Ala	Gly	Val	Tyr	Gly	Phe	Trp	Lys	Tyr	Val	
705					710					715					
TCT	AAA	CTA	GAG	AGA	AGA	GAG	ACA	CGA	CGT	TAT	CTT	GAG	ATG	TTC	2204
Ser	Lys	Leu	Glu	Arg	Arg	Glu	Thr	Arg	Arg		Leu	Glu	Met	Phe	
720					725	•				730					
				mme	oc.	~>m	cmc.	<b>CCC</b>	220	mcm	<del>ር</del> ሞጥ	CCC	CTTC	GCA	2249
			Lys												2247
735	TIE	neu	בענת	1116	740	ະເວັກ	Lu			745					

ACA	GAT	GAA	GAG	CCT	TCT	ACT	ACT	GAT	GCA	GTT	GCG	ACA	TTC	CGT	2294	
Thr	Asp	Glu	Glu	Pro	Ser	Thr	Thr	Asp	Ala	Val	Ala	Thr	Phe	Arg		
750					755					760						
						nm > 00	00100									
3GA	CCT	TGA	ACGC	TGCT	GC :	PTACI	rGAGG	r T	CAAC	5'T'T'G'!	l' GTA	ATATA	ATTA.		2343	
Sly	Pro	End														
CTGI	'GAAA	GG A	AATAA	GTGT	A G	CTACA	CAAA	AGG	TTCI	CAA	CTAT	TAG:	TAT		2393	
CTTC	TCTC	TG T	TAAAT	AACG	A G	AGTGA	AAAA	TGI	AATA	TTG	TTG	TGT	CTT		2443	
2222	АСТО	ag T	TTTGC	TTTG	יים יו	TATTI	מאדרי	GTG	TATO	ACA	ATAT	rgrai	CA		2493	
מידימיו	a ccc	:አጥ ጣ	rcttc	י א כבידיכב	ል ጥረ	דמידמי	מממרי	ממ	רים ביתי	CAC	СЪТС	יפאאר	יתיתי		2543	
ININ	an C G C	, ra -					. ~				0.,1				2313	
ላ አጥሮ	הגגר	mc (	2 A C A C	ב מאר	Δ										2563	

- These sequences can also be combined together in a suitable plasmid which leads to a combination of the individual characteristics, conditioned by the expression of the protein.
- 10 The promoter should ensure that the foreign gene is expressed in the plant. The promoter can be so chosen that the expression occurs only in specified tissues, at a determined time point in the plant's development or at a time point determined by outside influences. The promoter can be homologous or heterologous to the plant. Suitable promoters are e.g. the promoter of the 35S RNA of the cauliflower mosaic virus, the patatin promoter B33 (Rocha-Sosa et al. (1989) EMBO J 8: 23-29) or a promoter

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that ensures an expression only in photosynthetically active tissues. Other promoters can be used which ensure an expression only in specified organs, such as the root, tuber, seed, stem or specified cell types such as mesophyllic, epidermal or transport cells.

The coding sequences described herein contain the information for the formation of an mRNA for the large subunit of the ADP-glucose-pyrophosphorylase and the sucrose-phosphate-synthase (SPS) and a part of the 10 information for formation of the small subunit of the ADP-glucose-pyrophosphorylase as well as the sucrose-synthase, that are suitable for the formation of anti-sense RNA to the corresponding genes. Whether a translatable mRNA or an anti-sense nucleic acid is formed, 15 depends on the orientation of the coding sequence in relation to the promoter. If the 3' end of the coding sequence is fused to the 3' end of the promoter, an anti-sense RNA results, and by fusion of the 5' end of the coding to the 3' end of the promoter a translatable RNA 20 results. This latter leads to an increase of the enzyme activity in the cell, whilst the first leads to a reduction of the enzyme activity in the cell.

The coding sequence for the large and small subunit of the ADP-glucose-pyrophosphorylase, the sucrose phosphate synthase and the sucrose synthase can be one of those described in this invention or can be one that is derived by modifications of the sequences described above.

Thereby especially modifications of the sequences can be considered which lead to by-passing of the plant's own regulation mechanisms. Modifications to the DNA sequences of the invention can be by known methods, such as e.g. base exchange or targeted or non-targeted mutagenesis. The so-formed derivatives of the DNA sequences of the invention are also within the scope of the invention.

With plasmids, which contain one or more of the DNA sequences of the invention, sugar beet can be transformed with the object of raising and/or reducing the enzyme activity and/or the change of the sucrose concentration.

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For the introduction of the DNA sequences of the invention in sugar beet, a large number of cloning vectors are available, which contain a replication signal for *E. coli* and a marker, which allows a selection of the transformed cells.

According to the introduction method of the desired gene in the plant, other DNA sequences may be suitable. Should the Ti- or Ri-plasmid be used, e.g. for the transformation of the plant cell, then at least the right boundary, often 15 however both the right and left boundary of the Ti- and Ri-Plasmic T-DNA, is attached, as a flanking region, to the gene being introduced. The use of T-DNA for the transformation of plants cells has been intensively researched and is well described in EP 120 516; Hoekama, 20 In: The Binary Plant Vector System, Offset-drukkerij Kanters B.V. Alblasserdam, (1985), Chapter V; Fraley, et al., Crit. Rev. Plant Sci., 4:1-46 and An et al. (1985) EMBO J. 4: 277-287. Once the introduced DNA is integrated in the genome, it is as a rule stable there and remains 25 also in the offspring of the original transformed cells. It normally contains a selection marker, which induces resistance in the transformed plant cells against a biocide or antibiotic such as kanamycin, G 418, bleomycin, hygromycin or phosphinotricin etc. The individual marker 30 employed should therefore allow the selection of transformed cells from cells, which lack the introduced DNA.

For the introduction of DNA into a plant, besides transformation using Agrobacteria, there are many other

techniques available. These techniques include the fusion of protoplasts, microinjection of DNA and electroporation, as well as ballistic methods and virus infection. From the transformed plant material, whole plants can be regenerated in a suitable medium, which contains antibiotics or biocides for the selection. The resulting plants can then be tested for the presence of introduced DNA. No special demands are placed on the plasmids in injection and electroporation. Simple plasmids, such as e.g. pUC-derivatives can be used. Should however whole 10 plants be regenerated from such transformed cells the presence of a selectable marker gene is necessary. The transformed cells grow within the plants in the usual manner (see also McCormick et al. (1986) Plant Cell Reports 5: 81-84). These plants can be grown normally and crossed 15 with plants, that possess the same transformed genes or different. The resulting hybrid individuals have the corresponding phenotypical properties.

In order to understand the examples forming the basis of this invention all the processes necessary for these tests and which are known per se will first of all be listed:

# 25 1. Cloning process

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The vectors pUC 18/19 and M13mp10 series (Yanisch-Perron et al. (1985) Gene 33: 103-119), as well as the vector EMBL 3 (Frischauf et al. (1983) J Mol Biol 170: 827-842) were used for cloning.

For the plant transformations, the gene constructs were cloned in the binary vector BIN 19 (Bevan (1984) Nucl. Acids Res 12: 8711-8720)

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2. Bacte<u>rial strains</u>

The  $E.\ coli$  strain BMH71-18 (Messing et al., Proc. Natl. Acad. Sci. USA (1977), 24, 6342-6346) or TB1 was used for the pUC and M13 mP vectors.

- For the vector BIN19, the *E. coli* strain TB1 exclusively, was used. TB1 is a recombinant-negative, tetracycline-resistant derivative of strain JM101 (Yanisch-Perron et al., Gene (1985), 33, 103-119). The genotype of the TB1 strain is (Bart Barrel, personal communication):
- F'(traD36, proAB, lacI, lacZΔM15), Δ(lac, pro), SupE, thiS, recA, Sr1::Tn10(TcR).

The transformation of the plasmids into the potato plants was carried out using Agrobacterium tumefaciens strain

15 LBA4404 (Bevan, (1984), Nucl. Acids Res. 12, 8711-8720).

### 3. Transformation of Agrobacterium tumefaciens

In the case of BIN19 derivatives, the insertion of the DNA into the Agrobacterium was effected by direct transformation in accordance with the method of Holsters et al., (1978) (Mol Gene Genet 163: 181-187). The plasmid DNA of the transformed Agrobacterium was isolated in accordance with the method of Birnboim and Doly (1979)

(Nucl Acids Res 7: 1513-1523) and was analysed by gel electrophoresis after suitable restriction cleavage.

## 4. Sucrose phosphate-synthase activity test

- The sucrose phosphate-synthase activity was determined according to the method of Siegel and Stitt (1990, Plant Science 66: 205-210) in a two stage analysis. To 180  $\mu$ l of a solution of 50mM HEPES/KOH (pH 7.4), 5mM magnesium chloride, 5mM fructose-6-phosphate, 25mM
- glucose-6-phosphate and 6mM uridine-5'-diphosphoglucose, 20  $\mu l$  of probe was added and incubated for 10 minutes at

WO 94/28146 PCT/EP94/01671

38

25°C. It was heated for 3 minutes at 95°C, to complete the reaction. After centrifuging, the supernatant was spectroscopically analysed for the liberation of uridine-5'-diphosphate, whereby a pyruvate-kinase coupling enzyme reaction was used. Preparations without hexose phosphate, as well as the measurement of the recovery of added uridine-5'-diphosphate act as controls.

#### Examples

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#### Example 1

Cloning of cDNA to large and small subunits of the ADP glucose pyrophosphorylase of sugar beet.

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From the storage roots of 3-4 month old sugar beet plants grown in the greenhouse, RNA was isolated according to the method of Logemann et al (1987, Anal Biochem 163, 16-20). Resulting from poly-A+-RNA, a cDNA library was laid down according to the method of Gubler and Hoffmann (1983, Gene 25, 263) in the expression vector Lambda Zap II XR. To this there was used an oligo-dT primer provided with an XhoI recognising position and for synthesis of the first cDNA strand methylated cytidine nucleotide was inserted. After synthesis of the two strands an EcoRI-adaptor was attached and removed to one side by again cutting with the restriction endonuclease XhoI. In this way the hemimethylation of cDNA was hindered so that an internal XhoI recognition position is cut. By these procedures there is obtained a population of cDNA molecules, that can be cloned directed into the EcoRI/XhoI cut DNA of the phage Lambda. After packing of recombinant phage-DNA in phage heads, 200000 plaque forming units of the bank were plated out for infection of a bacterial colony and then each is probed with the total cDNA fragment of the large and/or subunit of the AGPase of potato (Müller-Roeber et

WO 94/28146 PCT/EP94/01671

39

al., 1990, MGG 224, 136-146) as an EcoRI-fragment. The recombinant phages corresponding to the hybridising signal were isolated. By in vivo excision plasmids were cut out from the Lambda zap-genome, which carry a double stranded cDNA as insertion. The plasmids were transformed in bacterial cells. The plasmid-DNA was then propagated in the bacteria. After checking the size of the insertions individual clones were analysed by determination of the primary sequence.

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#### Example 2

Cloning of cDNA to sucrose-phosphate-synthase (SPS) from sugar beet.

From the storage roots of 3-4 month old sugar beet plants grown in the greenhouse, RNA was isolated according to the method of Logemann et al (1987, Anal Biochem 163, 16-20). Resulting from poly-A+-RNA, a cDNA library was laid down 20 according to the method of Gubler and Hoffmann (1983, Gene 25, 263) in the expression vector Lambda Zap II XR. To this there was used an oligo-dT primer provided with an XhoI recognising position and for synthesis of the first cDNA strand methylated cytidine nucleotide was inserted. 25 After synthesis of the two strands an EcoRI-adaptor was attached and removed to one side by again cutting with the restriction endonuclease XhoI. In this way the hemimethylation of cDNA was hindered so that an internal XhoI recognition position is cut. By these procedures 30 there is obtained a population of cDNA molecules, that can be cloned directed into the EcoRI/XhoI cut DNA of the phage Lambda. After packing of recombinant phage-DNA in phage heads, 200000 plaque forming units of the bank were plated out for infection of a bacterial colony and then 35 each is probed with the total cDNA fragment of the

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sucrose-phosphate-synthase (SPS) from spinach (Sonnewald, 1992, Planta) as NotI. The recombinant phages corresponding to the hybridising signal were isolated. By in vivo excision plasmids were cut out from the Lambda zap-genome, which carry a double stranded cDNA as insertion. The plasmids were transformed in bacterial cells. The plasmid-DNA was then propagated in the bacteria. After checking the size of the insertions individual clones were analysed by determination of the primary sequence.

### Example 3

Cloning of cDNA to sucrose-synthase from sugar beet.

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From the storage roots of 3-4 month old sugar beet plants grown in the greenhouse, RNA was isolated according to the method of Logemann et al (1987, Anal Biochem 163, 16-20). Resulting from poly-A+-RNA, a cDNA library was laid down according to the method of Gubler and Hoffmann (1983, Gene 20 25, 263) in the expression vector Lambda Zap II XR. To this there was used an oligo-dT primer provided with an XhoI recognising position and for synthesis of the first cDNA strand methylated cytidine nucleotide was inserted. After synthesis of the two strands an EcoRI-adaptor was 25 attached and removed to one side by again cutting with the restriction endonuclease XhoI. In this way the hemimethylation of cDNA was hindered so that an internal XhoI recognition position is cut. By these procedures there is obtained a population of cDNA molecules, that can 30 be cloned directed into the EcoRI/XhoI cut DNA of the phage Lambda. After packing of recombinant phage-DNA in phage heads, 200000 plaque forming units of the bank were plated out for infection of a bacterial colony and then parallel is probed with both EcoRI/BgIII sub fragments sucrose synthase from maize (Worrell et al., 1991, Plant

Cell 3, 1121-1130). The recombinant phages corresponding to the hybridising signal were isolated. By in vivo excision plasmids were cut out from the Lambda zap-genome, which carry a double stranded cDNA as insertion. The plasmids were transformed in bacterial cells. The plasmid-DNA was then propagated in the bacteria. After checking the size of the insertions individual clones were analysed by determination of the primary sequence.

#### 10 Example 4

Determination of the nucleotide sequence of the ADP glucose pyrophosphorylase, the sucrose synthase and the sucrose phosphate synthase of sugar beet and derivation of

15 the corresponding amino acid sequences

The nucleotide sequences of the insertions obtained from Examples 1 -3, were determined by standard methods by means of the dideoxy method (Sanger et al. (1977) Proc.

Natl. Acad. Sci. USA, 74, 5463-5467). The nucleotide sequences and the amino acid sequences derived therefrom are given in the sequence protocols Seq. ID No. 1-4.

The sequences are shown earlier; the protocols are as follows:

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#### SEO ID NO: 1

SEQUENCE TYPE: Nucleotide with corresponding protein.

SEQUENCE LENGTH: 1924 base pairs

5 STRANDEDNESS: single

TOPOLOGY: linear MOLECULE TYPE: cDNA

ORIGINAL SOURCE

10 ORGANISM: Beta vulgaris

IMMEDIATE EXPERIMENTAL SOURCE: cDNA library in Phage Lamda

zap

#### FEATURES:

15 from 206 to 1770 coding region

PROPERTIES: ADP-glucose-pyrophosphorylase, large subunit

#### SEO ID NO: 2 20

SEQUENCE TYPE: Nucleotide with corresponding protein

SEQUENCE LENGTH: 1763 base pairs

STRANDEDNESS: single

25 TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: Beta vulgaris

IMMEDIATE EXPERIMENTAL SOURCE: cDNA library in Phage Lamda 30

zap

#### FEATURES:

from 3 to 1469 coding region

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PROPERTIES: ADP-glucose-pyrophosphorylase, small subunit

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SEQ ID NO: 3

SEQUENCE TYPE: Nucleotide with corresponding protein .

SEQUENCE LENGTH: 3635 base pairs

5 STRANDEDNESS: single

TOPOLOGY: linear MOLECULE TYPE: cDNA

ORIGINAL SOURCE

10 ORGANISM: Beta vulgaris

IMMEDIATE EXPERIMENTAL SOURCE: cDNA library in Phage Lamda

zap

FEATURES:

15 from 31 to 3164 coding region

PROPERTIES: Sucrose-phosphate-synthase

20 <u>SEO ID NO: 4</u>

SEQUENCE TYPE: Nucleotide with corresponding protein

SEQUENCE LENGTH: 2563 base pairs

STRANDEDNESS: single

25 TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: Beta vulgaris

30 IMMEDIATE EXPERIMENTAL SOURCE: cDNA library in Phage Lamda

zap

FEATURES:

from 3 to 2300 coding region

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PROPERTIES: Sucrose synthase

### CLAIMS

DNA sequence with the coding region for die large subunit of ADP-glucose-pyrophosphorylase for the preparation of sugar beet with changed sucrose concentration, characterised in that the sequence has the following nucleotide sequence (Seq. ID No.1):

CAAAAGAAAA ACTTCCCATT TCTACTTCTT TGCACAATAT AATTTCCCAC	0050
CAATTTTTCT TTAAATTTCT CACTTTCATT TAATCAGTTT TCAGCAACAT	0100
TCTGATACTC GACAACCCAC TTTCTGTTCT CCCAAGATTC CAAACCTCTG	0150
ATTCTCATTC CACTAATATT TTTGCTTATT TTTTTTCTGG ATTTAAAGAA	0200
AAGCT ATG GAT GCA AGT GCA GCA GCC ATA AAT GTC AAT GCC CAT  Met Asp Ala Ser Ala Ala Ala Ile Asn Val Asn Ala His  5 10	0243
TTA ACA GAA GTT GGA AAG AAA CGT TTT TTA GGA GAG AGA ATC AGT Leu Thr Glu Val Gly Lys Lys Arg Phe Leu Gly Glu Arg Ile Ser 15 20 25	0288
CAA AGT TTG AAG GGT AAA GAT CTG AGA GCT CTG TTT TCA AGA ACT Gln Ser Leu Lys Gly Lys Asp Leu Arg Ala Leu Phe Ser Arg Thr 30 35 40	0333
GAG AGC AAG GGT AGA AAT GTC AAT AAA CCT GGG GTT GCA TTT TCT Glu Ser Lys Gly Arg Asn Val Asn Lys Pro Gly Val Ala Phe Ser 45 50 55	0378
GTT CTC ACC TCA GAT TTT AAT CAA AGT GTT AAA GAA TCT TTG AAA Val Leu Thr Ser Asp Phe Asn Gln Ser Val Lys Glu Ser Leu Lys 60 65 70	0423

mam	CAC	CCA	GCA	መጥ አ	ጥጥጥ	CAA	ጥርጥ	CCA	444	CCT	GAC	CCA	מממ	ידעע	0468
															0400
Tyr		Pro	Ala	Leu	Pne		ser	Pro	гÀг	Ala		Pro	гĀг	Asn	
	75					80					85				
GTG	GCT	GCÀ	ATT	GTG	CTG	GGT	GGT	GGT	GCT	GGG	ACT	CGC	CTC	TTT	0513
Val	Ala	Ala	Ile	Val	Leu	Gly	Gly	Ġly	Ala	Gly	Thr	Arg	Leu	Phe	
	90					95					100				
CCT	CTT	ACT	AGC	AGG	AGA	GCT	AAG	CCA	GCA	GTG	CCA	ATT	GGA	GGG	0558
Pro	Leu	Thr	Ser	Arq	Arg	Ala	Lys	Pro	Ala	Val	Pro	Ile	Gly	Gly	
	105			-	•	110	_				115				
	100														
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			Leu												
Cys	_	Arg	Leu	TIE	Asp		FIU	Mec	Der		130	110	non	001	
	120					125					130				
			AAG												0648
Gly	Ile	Arg	Lys	Ile	Phe	Ile	Leu	Thr	Gln	Phe	Asn	Ser	Phe	Ser	
	135					140					145				
CTT	AAT	CGT	CAT	CTT	GCT	CGA	ACC	TAT	AAT	TTT	GGA	GAT	GGT	GTG	0693
Leu	Asn	Arg	His	Leu	Ala	Arg	Thr	Tyr	Asn	Phe	Gly	Asp	Gly	Val	
	150					155					160				
አአጥ	יווייוייוי	ccc	СУТ	GGC	ጥጥጥ	GTG	GAG	GTT	ттт	GCT	GCT	ACA	CAA	ACA	0738
			Asp												- /
ASN		GTÅ	woh	GIY	FIIC		Gru	*47	1116		175				
	165					170					113				

			TCA												0783
Pro	Gly	Glu	Ser	Gly	Lys	Lys	Trp	Phe	Gln	Gly	Thr	Ala	.Asp	Ala	
	180					185					190				
GTA	AGA	CAG	TTT	TTC	TGG	GCA	TTT	GAG	GAT	TCC	AAA	TCC	AAG	GAT	0828
Val	Arg	Gln	Phe	Phe	Trp	Ala	Phe	Glu	Asp	Ser	Lys	Ser	Lys	Asp	
	195					200					205				
													٠		
GTC	GAG	CAT	ATA	GTT	ATT	TTA	TCC	GGT	GAT	CAT	CTT	TAC	CGA	ATG	0873
Val	Glu	His	Ile	Val	Ile	Leu	Ser	Gly	Asp	His	Leu	Tyr	Arg	Met	
	210					215					220				
GAT	TAC	ATG	AGT	TTT	TGG	CAG	AAG	CAC	ATT	GAC	ACC	AAT	GCT	GAT	0918
Asp	Tyr	Met	Ser	Phe	Trp	Gln	Lys	His	Ile	Asp	Thr	Asn	Ala	Asp	
-	225					230					235				
ATT	ACA	GTG	TCA	TGC	ATA	ccc	ATG	GAT	GAC	AGC	CGT	GCA	TCG	GAT	0963
Ile	Thr	Val	Ser	Cys	Ile	Pro	Met	Asp	Asp	Ser	Arg	Ala	Ser	Asp	
	240					245					250				
TAT	GGG	CTG	ATG	AAG	ATT	GAT	CAC	ACT	GGA	CGC	ATT	GTC	CAT	TTT	1008
			Met												
- 1 -	255			-		260					265				
GCA	GAA	AAA	ccc	AAG	GGT	TCT	GAT	CTA	ACA	GCA	ATG	CAA	GTA	GAT	1053
			Pro												
	270	-, -			-	275	•				280				
	2.0														

ACA	ACT	GTT	CTT	GGG	CTC	TCT	GAC	CTT	GAA	GCT	ATG	TCA	AAT	CCA	1098
Thr	Thr	Val	Leu	Gly	Leu	Ser	Asp	Leu	Glu	Ala	Met	Ser	Asn	Pro	
	285					290					295				
TAT	ATT	GCA	TCA	ATG	GGT	GTT	TAT	ĠTC	TTT	CGA	ACG	GAT	GTT	CTT	1143
Tyr	Ile	Ala	Ser	Met	Gly	Val	Tyr	Val	Phe	Arg	Thr	Asp	Val	Leu	
	300					305					310				
ATG	GAG	CTT	CTC	AAT	CGA	AAA	TAC	CCT	TCA	AGC	AAT	GAT	TTT	GGC	1188
Met	Glu	Leu	Leu	Asn	Arg	Lys	Tyr	Pro	Ser	Ser	Asn	Asp	Phe	Gly	
	315					320					325				
											AAT				1233
Ser		Ile	Ile	Pro	Ser		Val	GIY	Glu	ser	Asn	Val	Gln	Ala	
	330					335					340				
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											Thr				1276
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	343					330					555				
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											Pro				
	360					365					370		•		
GAA	TTC	TAC	GAT	CCA	AAA	ACA	CCT	TTT	TAT	ACA	TCT	GCA	AGA	TTT	1368
Glu	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Tyr	Thr	Ser	Ala	Arg	Phe	
	375					380	•				385				

														WII	1413
Leu	Pro	Pro	Thr	Lys	Val	Asp	Arg	Cys	Lys	Ile	Val	Asp	Ser	Iļe	
	390					395					400				
GTA	TCC	CAT	GGT	TGT	TTT	CTA	CAG	GAG	TCT	AGC	ATC	CAA	CAT	TCC	1458
			Gly												
	405		_			410					415				
<u>አ</u> ጥጥ	стт	GGT	GTT	CGC	TCA	AGA	TTA	GAG	TCC	GGG	GTT	GAG	TTC	CAG	1503
			Val												
	420			,		425					430				
	420														
GAC	» CC	ATG	ATG	ATG	GGC	GCA	GAT	TAC	TAT	CAA	ACT	GAA	TCA	GAA	1548
			Met												
rsp	435			•••	2	440	-	-	_		445				
	433														
ע תייחי	CCT	ጥርጥ	CTG	СТТ	GCT	GAG	GGA	AAG	GTT	CCT	GTT	GGT	GTC	GGA	1593
			Leu												
116	450	001				455	•	-			460				
	430														
CAC	አአጥ	NCC.	מממ	מידמ	AAG	AAT	TGC	ATA	ATT	GAC	AAG	AAC	GCC	AAA	1638
			Lys												
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	465					,,,			•						
> mm	663	777	CNM	GT/G	CT A	ътс	GCA	AAC	ACG	GAT	GGT	GTT	GAG	GAA	1683
ATT	GGA	AAA	Asp	3757	GIM	Tlo	בומ	) en	Thr	Asn	Glv	Val	Glu	Glu	
lle			Asp	val	val	485	WYG	лэн			490				
	480					400					470				

GCA	GAT	AGA	CCA	AAT	GAA	GGC	TTT	TAC	ATC	AGG	TCG	GGC	ATT	ACC	1728
Ala	Asp	Arg	Pro	Asn	Glu	Gly	Phe	Tyr	Ile	Arg	Ser	Gly	Ile	Thr	
	495					500					505				
														TAG	1773
TTE	510	Leu	Lys	ASN	Ala	515	116	GIII	ASP	GIY	520	Val	TIE	Lna	
	210					J13					320				
ATT:	TAAT	CAT A	AACCI	CATI	ra ga	AAAG?	LAAT	ATT	TTG	CATG	ATTI	CCTI	TTT		1823
CAT	TAAC	CT A	AAACI	GGCI	TA A	ACCAC	GAG	TTI	TCT	CATC	TGT	TATA	ATA		1873
ATA:	rgtci	'AT A	ACTA	YTGG?	AA TA	ATCTI	AATA	AAA	LAAAA	AAA	AAAA	AAAA	LAA		1923
															1924
A													•		1724
2.	DN	A se	guen	ce w	ith	the	codi	ng r	egio	n fo	r th	e sm	all	subun	it of the
	AD	P-gl	ucos	е-ру	roph	osph	alas	e fo	r th	e pr	epar	atio	n of	suga	r beet
	wi	th c	hang	ed s	ucro	se c	once	ntra	tion	, ch	arac	teri	sed	in th	at the
	se	quen	ce h	as t	he f	ollo	wing	nuc	leot	ide	sequ	ence	(Se	q. ID	No.2):
						_ 0_						.0.			
GG			GTG												0044
	Ile	Thr	Val	Pro	Ser 5	Thr	ser	Ser	гÀг	Asn 10	Leu	GIN	Asn	Ser	
					5					10					
стс	GCA	ттс	TCC	тст	тст	TCT	CTC	TCC	GGC	GAC	AAA	ATT	CAA	ACG	0089
			Ser												
15					20	•			_	25					
ACG	TCA	TTT	CTC	AAC	CGC	CGA	TAT	TGT	AGA	ATC	тст	TCT	AGA	GCT	0134
Thr	Ser	Phe	Leu	Asn	Arg	Arg	Tyr	Cys	Arg	Ile	Ser	Ser	Arg	Ala	
30					35					40					

CCG	ATT	GTT	GTC	TCT	ccc	AAA	GCT	GTT	TCT	GAT	TCT	AAG	TAA	TCG	0179
Pro	Ile	Val	Val	Ser	Pro	Lys	Ala	Val	Ser	Asp	Ser	Lys	Asn	Ser	
45					50					55					
		TGT													0224
Gln	Thr	Cys	Leu	Asp	Pro	Glu	Ala	Ser	Arg	Ser	Val	Leu	Gly	Ile	
60					65					70					
															0060
		GGA													0269
Ile	Leu	Gly	Gly	Gly		Gly	Thr	Arg	Leu		Pro	Leu	Thr	Lys	
75					80					85					
3 3 C	262	GCC	אאא	CCA	GCC	GTG	CCA	ርጥር	GGT	GCT	ТАА	ТАТ	AGG	CTT	0314
		Ala													
90 2	Arg	AIG	Буз	110	95	,,,			1	100		-1-	3		
90															
ATT	GAT	ATC	CCA	GTG	AGC	AAT	TGT	TTG	AAC	AGT	AAT	ATT	TCC	AAA	0359
Ile	Asp	Ile	Pro	Val	Ser	Asn	Cys	Leu	Asn	Ser	Asn	Ile	Ser	Lys	
105					110					110					
									C O.T.	mom	ome	3 3 CC	CCTT	C N M	0404
		GTT													0404
	Tyr	Val	Leu	Thr		Pne	ASN	Ser	Ala	125	Leu	ASII	ALG	urs	
115					120					125					
СПП	TCG	CGG	GCA	TAT	GCT	AGC	AAC	ATG	GGA	GGA	TAC	AAA	TAA	GAG	0449
		Arg													
130		_		_	135					140					
						•									
		GTA													0494
Gly	Phe	Val	Glu	Val	Leu	Ala	Ala	Gln	Gln	Ser	Pro	Glu	Asn	Pro	
145					150					155					

										AGG Arg 170					0539
									Tyr	TTG Leu 185			•		0584
									Arg	TTT Phe 200					0629
										GCA Ala 215					0674
									Met	AAA Lys 230				GAA Glu	0719
GGA Gly										AAA Lys 245				TTG Leu	0764
					GAT					GGT					0809
Lys 250	Ala	Met	Lys	Val	Asp 255	Thr	Thr	Ile	Leu	Gly 260	Leu	qaA	Asp	G 1,11	

AGA	GCA	AAA	GAA	ATG	CCA	TTC	ATA	GCC	AGC	ATG	GGC	ATA	TAT	GTT	0854
Arg	Ala	Lys	Glu	Met	Pro	Phe	Ile	Ala	Ser	Met	Gly	Ile	Tyr	Val	
265					270					275					
ATT	AGC	AAA	GAT	GTA	ATG	CTT	AAT	CTG	CTT	CGG	GAG	CAA	TTT	CCT	0899
Ile	Ser	Lys	Asp	Val	Met	Leu	Asn	Leu	Leu	Arg	Glu	Gln	Phe	Pro	
280		_			285					290					
GGT	GCT	AAT	GAT	TTT	GGA	AGT	GAA	GTT	ATT	CCA	GGC	GCC	ACT	TCC	0944
										Pro					
295			-		300					305					
ATA	GGG	TTG	AGA	GTC	CAA	GCT	TAT	TTG	TAT	GAT	GGT	TAC	TGG	GAG	0989
										Asp					
310	-				315					320					
GAT	ATT	GGT	ACC	ATT	GAA	GCT	TTT	TAC	AAT	GCT	AAC	TTG	GGA	ATC	1.054
Asp	Ile	Gly	Thr	Ile	Glu	Ala	Phe	Tyr	Asn	Ala	Asn	Leu	Gly	Ile	
325					330					335					
ACC	AAA	AAG	CCG	GTG	CCA	GAT	$\mathbf{T}\mathbf{T}\mathbf{T}$	AGC	TTC	TAT	GAT	CGT	TCA	TCT	1079
Thr	Lys	Lys	Pro	Val	Pro	Asp	Phe	Ser	Phe	Tyr	Asp	Arg	Ser	Ser	
340					345					350					
CCA	ATT	TAT	ACA	CAA	CCT	CGG	TAT	TTG	CCT	CCT	TCA	AAG	ATG	CTT	1124
										Pro					
355		-			360	•				365					

			ATA Ile												1169
370					375					380					
			AAG												1214
Lys 385	Asn	Cys	Lys	Ile	His 390	His	Ser	Val		G1y 395	Leu	Arg	Ser	cys	
			GGT												1259
Ile	Ser	Glu	Gly	Ala	Ile	Ile	Glu	Asp	Thr		Leu	Met	Gly	Ala	
400					405					410					
															1204
			GAG												1304
Asp	Tyr	Tyr	Glu	Thr		Ala	Asp	Arg	Lys	425	Leu	Ala	Ald	гуs	
415					420					425					
							222		663	ccm	እመመ	CCC	ር አጥ	CAT	1349
			CCT												1343
-	Ser	Val	Pro	TIE	435	TIE	GIY	ASII	ATG	440	116	Gry	nop	p	
430					433					440					
					3.CM	CAC	አአጥ	Cm x	CNA	CAA	GCA	GCA	AGA	GAA	1394
														Glu	
		TIE	TIE	ASII	450	ASP	No.	741	<b>U</b> 1	455			<b>J</b>		
445					-150										
	<b></b>		m > C	mm.c	א מוזי ע	. אמ	ልርር	GGA	ልጥል	<b>G</b> ጥር	ACT	АТА	ATC	AAG	1439
ACA	GAC	GGA	TAC	Dhe	TIP	Tive	Ser	Glv	Ile	Val	Thr	Ile	Ile	Lys	
		GIÀ	туг	File	465	ב ציב	DCL	Cry		470				4	
460															

			ATT Ile	Pro	Ser				Ile	End	AAAT	GGAG	CA	•	1482
475					480					485					
TATA	ATA.	AT I	TCAC	CTGCC	T AT	ATT	CAGT	A· CCI	TATCT	rgag	TCTC	CCAC	CA		1532
TGAC	CCTI	TG P	ATTC#	ATCI	T T	'AGT'	ratg:	AAA 1	TAT	TTTT	GGCT	TTTG	CG		1582
ATTI	TGCC	CAT A	LTAAL	rtgaa	G A	AGCG	AGGA:	r TC?	\GGG?	ACGA	TAGI	GCTA	TG		1632
AATT	GGA	AGA A	\AGG <i>I</i>	TTTC	G GC	GAT	ATCT:	r TG1	)AAA	GACA	TTTT	GACT	'AC		1682
TGGG	CACI	CAA A	LAAT	rtggi	A A	rgct	ATAC	C AAA	'ATA!	ГАТА	AAAA	GATC	TT		1732
GCT	GGTI	TTT (	GTA!	AAAA	A AA	AAAA	AAAA	A A							1763
	3.										_			_	
	٥.	ŗ	hosp	hate	. <b>-</b> s	yntl	nase		the	prep	arat	ion		ugar	
	٠.	r	hosp eet	ohate with	e - s	ynt) inge	nase d sud	for crose	the cor	prep ncent	arat rati	ion on,	of s	ugar	ina
5	٠.	r c	hosp eet	ohate with	- s cha	yntl inged l in	nase d suc that	for crose t the	the cor	prep ncent quenc	arat rati e ha	ion on,	of s		ing
		r k c	ohosp beet chara nucle	ohate with acter	e - s cha ised	ynth inged in equei	nase d suc that nce	for crose t the (Seq.	the cor sec	prepocent quenc	arat rati e ha	ion on, s th	of s	ugar	ing 0044
		r k c	ohosp beet chara nucle	ohate with acter	e - s cha ised	ynth inged in eque	nase d suc that nce	for crose t the (Seq.	the cor sec ID	preposent prepos	erati e ha	ion on, s th GAT Asp	of s	ugar	
		r k c	ohosp beet chara nucle	ohate with acter	e - s cha ised	ynth inged in eque	nase d suc that nce	for crose t the (Seq.	the cor sec ID	preposent prepos	eratice has):	ion on, s th	of s	ugar	
GGGG	CTGC!	i d o n AGG	ohosp oeet chara nucle GAAGO	ohate with acter cotic	e - s cha ised de se GA A	synth inged in equer CTTC	nase d suc that nce AAAA	for crose the (Seq. ATG Met	the core second ID	prepose of the property of the	caratice has: AAT ASD	ion on, s th GAT Asp 5	of s	ugar llow:	
GGGG	CTGC!	i d o n AGG	ohosp oeet chara nucle GAAGO	ohate with acter cotic	e - s cha ised de se GA A	synth inged in equer CTTC	nase d suc that nce AAAA	for crose the (Seq. ATG Met	the core second ID	prepose of the property of the	eratice has):  AAT Asn	ion on, s th GAT Asp 5	of s	llow: GGA Gly	0044
GGGG	CTGC!	i d o n AGG	ohosp oeet chara nucle GAAGO	ohate with acter cotic	e - s cha ised de se GA A	synth inged in equer CTTC	nase d suc that nce AAAA	for crose the (Seq. ATG Met	the core second ID	preposent properties of the pr	caratice has: AAT ASD	ion on, s th GAT Asp 5	of s	ugar llow:	0044
GGGG TGG Trp	ATA Ile	AGG (AAC	ohosp beet chara nucle GAAGO AGT Ser	TAT Tyr 10	e - s charised de sa GA AG TTA Leu	synthinged in in equer CTTC	nase d suc that nce AAAA GCA Ala	for crose the (Seq. ATG Met ATT Ile	the core second ID  GCG Ala  CTG Leu 15	prepose of the property of the	caratice has: AAT ASN GTG Val	GAT Asp 5 GGT Gly	of s e fo	GGA Gly 20	0044
TGG Trp	ATA Ile	AGG (AACA)	ohosp beet chara nucle GAAGG AGT Ser	TAT Tyr 10	t - s charised de se GA AG TTA Leu	gAG Glu	nase id such that nce AAAA GCA Ala	for crose the (Seq. ATG Met ATT Ile	the core second ID GCG Ala CTG Leu 15	prepose of the property of the	caratice has: AAT ASD	on, s th  GAT Asp 5 GGT Gly	of see for contract of the con	GGA Gly 20	0044

$\mathbf{r}\mathbf{r}$	AGT	CCT	ACT	CGT	TAC	TTT	GTT	GAA	GAA	GTT	ATC	ACT	GG.T.	TTT	01/9
?he	Ser	Pro	Thr	Arg	Tyr	Phe	Val	Glu	Glu	Val	Ile	Thr	Gly	Phe	
				40					45					50	
GAT	GAA	ACC	GAC	CTT	CAT	CGT	TCA	TGG	GTT	CGG	GCA	CAA	GCA	ACA	0224
													Ala		
			-	55					60					65	
AGG	AGT	CCT	CAA	GAG	AGG	AAT	ACT	AGA	TTG	GAG	AAC	ATG	TGT	TGG	0269
													Cys		
arg	DCI			70	3			•	75					80	
<b>3</b> C 3	y ana	TGG	ידעע	ጥጥር	CCT	ССТ	CAG	AAG	AAG	CAG	CTT	GAG	ААТ	GAA	0314
													Asn		
arg	116	тър	ASII	85	AIU	n- 9	01	ביינב	90					95	
				65					,,,						
<b></b>	com	<b>6</b> 3.0	ccc	ስ ስ C	מרמ	277	ССТ	CGT	ATG.	GAG	СТТ	GAG	AGG	GGT	0359
													Arg		
GIU	Ala	GIN	Arg	100	TIIL	Буз	nr 9	n. 9	105	010				110	
				100					100						
		<b></b>	CON	3 CM	CCT	CAT	איזיכ	ምሮር	GAG	GAC	ጥጥΔ	TCA	GAA	GGC	0404
														Gly	
Arg	Arg	GIU	Ala		Ald	MSP	nec	361	120	пор	200	001		125	
				115					120						
				mo.	COM	CATE	CCT	ር አጥ	እርር	A CC	ССТ	ССТ	AGA	TTG	0449
GAA	AAG	GAC	Y.II.	TCA	GCT	CAT	661	GAI	AGC	mbr.	λνα	Dro	Ara	Len	• • • • •
Glu	Lys	Asp	Ile		Ala	HIS	GIÀ	ASP		1111	AT G	FIO	ni 9	Leu 140	
				130					135					140	
						a		3.000	C3.C	303	mc c	ን መጠ	אכיתי	C	0494
CCA	AGA	ATA	AAT	TCT	CTT	GA'I	GCT	ATG	GAG	ACA	166	ATT	BG1	CAA	049
Pro	Arg	Ile	Asn	Ser	Leu	Asp	Ala	Met		rnr	Trp	TIE	ser	Gln	
				145					150					155	

CAA	AAG	GAA	AAA	AAA	CTC	TAC	CTT	GTT	TTG	ATA	AGT	CTT	CAT	GGT	0539
Gln	Lys	Glu	Lys	Lys	Leu	Tyr	Leu	Val	Leu	Ile	Ser	Leu	His	Gly	
				160					165					170	
TTG	ATA	CGA	GGT	GAA	AAC	ATG	GAA	CTT	GGC	CGT	GAT	TCT	GAT	ACT	0584
Leu	Ile	Arg	Gly	Glu	Asn	Met	Glu	Leu	Gly	Arg	Asp	Ser	Asp	Thr	
				175					180					185	
		CAG													0629
Gly	Gly	Gln	Val	Lys	Tyr	Val	Val	Glu	Leu	Ala	Arg	Ala	Leu	Gly	
				190					195					200	
		CCA													0674
Ser	Met	Pro	Gly	Val	Tyr	Arg	Val	Asp	Leu	Leu	Thr	Arg			
				205					210					215	
													-1-		0710
		CCT													0719
Ser	Ser	Pro	Asp	Val	Asp	Trp	Ser	Tyr		Glu	Pro	Thr	GIA		
				220					225					230	
									a	<b>G.N.</b>	C N III	CAM	CAT	C	0764
		CCA													0704
Leu	Asn	Pro	Arg		Ser	Asn	GIY	Pne		Asp	Asp	Asp	ASP	245	
				235					240					243	
		GAG	አርጥ	א כייי	GGT	CCT	ጥልሮ	<u>አ</u> ጥጥ	ርጥጥ	CGT	ΑΤΑ	CCA	TTT	GGG	0809
		GAG													
Met	GIÀ	GIU	Set		СТУ	N1G	- 7 -		255	4				260	
				250					ررے						

CCG	AGG	GAT	AAG	TAT	ATC	GCA	AAA	GAA	GAG	CTT	TGG	CCC	TAT	ATT	0854
Pro	Arg	Asp	Lys	Tyr	Ile	Ala	Lys	Glu	Glu	Leu	Trp	Pro	Tyr	Ile	
				265					270					275	
CCT	GAA	TTT	GTT	GAT	GGT	GCT	CTA	AAC	CAC	ATA	GTT	CAA	ATG	TCC	0899
Pro	Glu	Phe	Val	Asp	Gly	Ala	Leu	Asn	His	Ile	Val	Gln	Met	Ser	
				280					285					290	
AAA	GTT	TTA	GGT	GAG	CAA	ATT	GGT	AGC	GGG	GAA	ACA	GTT	TGG	CCA	0944
Lys	Val	Leu	Gly	Glu	Gln	Ile	Gly	Ser	Gly	Glu	Thr	Val	Trp	Pro	
				295					300					305	
GTT	GCC	ATT	CAT	GGA	CAT	TAT	GCT	GAT	GCT	GGT	GAT	TCT	GCT	GCT	0989
Val	Ala	Ile	His	Gly	His	Tyr	Ala	Asp	Ala	Gly	Asp	Ser	Ala	Ala	
				310					315					320	
				310					315					320	
CTT	CTT	TCT	GGT		CTA	AAT	GTT	CCA		CTT	TTA	ACG			1034
			GGT Gly	GGC					ATG				GGG	CAT	1034
				GGC					ATG				GGG Gly	CAT	1034
				GGC Gly					ATG Met				GGG Gly	CAT His	1034
Leu	Leu	Ser	Gly	GGC Gly 325	Leu	Asn	Val	Pro	ATG Met 330	Leu	Leu	Thr	GGG Gly	CAT His 335	
Leu TCT	Leu	Ser	Gly CGA	GGC Gly 325 GAC	Leu AAG	Asn TTA	Val	Pro CAG	ATG Met 330	Leu	Leu AAA	Thr	GGG Gly GGT	CAT His 335	
Leu TCT	Leu	Ser	Gly	GGC Gly 325 GAC	Leu AAG	Asn TTA	Val	Pro CAG	ATG Met 330	Leu	Leu AAA	Thr	GGG Gly GGT	CAT His 335	
Leu TCT	Leu	Ser	Gly CGA	GGC Gly 325 GAC	Leu AAG	Asn TTA	Val	Pro CAG	ATG Met 330	Leu	Leu AAA	Thr	GGG Gly GGT	CAT His 335	
Leu TCT	Leu	Ser	Gly CGA	GGC Gly 325 GAC Asp	Leu AAG	Asn TTA	Val	Pro CAG	ATG Met 330 CTC Leu	Leu	Leu AAA	Thr	GGG Gly GGT	CAT His 335 CGA Arg	
Leu TCT Ser	Leu CTT Leu	Ser GGC Gly	Gly CGA Arg	GGC Gly 325 GAC Asp 340	Leu AAG Lys	Asn TTA Leu	Val GAG Glu	Pro CAG Gln	ATG Met 330 CTC Leu 345	Leu CTC Leu	Leu AAA Lys	Thr CAG Gln	GGG Gly GGT Gly	CAT His 335 CGA Arg 350	
TCT Ser	CTT Leu	GGC Gly	Gly CGA Arg	GGC Gly 325 GAC Asp 340	AAG Lys	TTA Leu AAC	Val GAG Glu AAT	Pro CAG Gln	ATG Met 330 CTC Leu 345	CTC Leu	AAA Lys ATA	Thr CAG Gln ATG	GGG Gly GGT Gly	CAT His 335 CGA Arg 350	
TCT Ser	CTT Leu	GGC Gly	Gly CGA Arg	GGC Gly 325 GAC Asp 340	AAG Lys	TTA Leu AAC	Val GAG Glu AAT	Pro CAG Gln	ATG Met 330 CTC Leu 345	CTC Leu	AAA Lys ATA	Thr CAG Gln ATG	GGG Gly GGT Gly	CAT His 335 CGA Arg 350	1079
TCT Ser	CTT Leu	GGC Gly	Gly CGA Arg	GGC Gly 325 GAC Asp 340	AAG Lys	TTA Leu AAC	Val GAG Glu AAT	Pro CAG Gln	ATG Met 330 CTC Leu 345	CTC Leu	AAA Lys ATA	Thr CAG Gln ATG	GGG Gly GGT Gly	CAT His 335 CGA Arg 350	1079

ATA	GAA	GCC	GAA	GAG	TTA	TCA	CTT	GAT	GCC	TCT	GAG	ATA	GTC	ATA	1169
Ile	Glu	Ala	Glu	Glu	Leu	Ser	Leu	Asp	Ala	Ser	Glu	Ile	Val	Ile	
				370					375					380	
ACT	AGT	ACA	AGA	CAA	GAA	ATA	GAA	GAG	CAA	TGG	CAC	CTC	TAT	GAT	1214
		Thr													
				385					390					395	
GGG	ጥጥጥ	GAT	ССТ	GTG	CTA	GAA	CGT	AAA	CTC	CGT	GCT	AGG	ATG	AAG	1259
		Asp													
Gry	1			400				•	405	•				410	
ССТ	GGT	GTA	AGC	тст	TAT	GGA	AGG	TTC	ATG	ccc	CGG	ATG	GTT	GTT	1304
		Val													
AI 9	Gry	· · · ·	001	415	-1-	2			420		_			425	
<u>አ</u> ጥጥ	ССТ	CCT	GGA	ATG	GAA	TTC	AAT	CAT	ATT	GTT	CCA	CAT	GAG	GGT	1349
		Pro													
116	110	110		430					435					440	
				,,,,											
										•					
C N M	አጥሮ	GAT	CCT	CAA	ACA	GAA	GAA	ACT	GAA	GAG	CAT	CCT	ACA	TCA	1394
		Asp													
Asp	Mec	ASP	Gly	445					450					455	
				443											
0.00	~ x m	CCA	CCT	δω√	ጥርር	ССФ	GAG	ልጥጥ	ATG	CGC	TTC	ттт	TCT	AAA	1439
		Pro													
Pro	Asp	Pro	PEO		тър	A10	GIU	116	465	••• 9				470	
				460					703					- · ·	

CCA	AGG	AAG	CCA	ATG	ATA	CTT	GCC	CTT	GCT	AGG	CCT	GAC	CCG	AAG	1484
Pro	Arg	Lys	Pro	Met	Ile	Leu	Ala	Leu	Ala	Arg	Pro	Asp	Pro	Lys	
				475					480					485	
														CCA	1529
Lys	Asn	Ile	Thr	Thr	Leu	Val	Lys	Ala	Phe	Gly	Glu	Cys	Arg	Pro	
				490					495					500	
					AAT										1574
Leu	Arg	GIU	Leu		Asn	Leu	Thr	ren		Met	GIÀ	ASI	_	_	
				505					510					515	
GGT	АТТ	GAC	GAG	ATG	TCA	AGC	ACC	AGT	тст	TCA	GTT	CTC	CTG	TCA	1619
					Ser										
3				520					525					530	
GTG	CTT	AAG	CTA	ATT	GAT	CAA	TAC	GAC	CTT	TAT	GGT	CAA	GTA	GCA	1664
Val	Leu	Lys	Leu	Ile	Asp	Gln	Tyr	Asp	Leu	Tyr	Gly	Gln	Val	Ala	
				535					540					545	
					AAG										1709
Tyr	Pro	Lys	His		Lys	Gln	Ala			Pro	Glu	Ile			
				550					555		•			600	
mm -		663		202	B B C	CCN	CTC	mmm	N ITO	አአጠ	CC3	ccm	നനന	አመጣ	1754
					AAG										1754
ьeu	ATG	Ald	гÃг	605	Lys	етй	vaı		610	יייפא	OLA	WIG		11e 615	
				005					910					013	

GAG	CCA	TTT	GGG	CTG	ACT	CTA	ATA	GAG	GCA	GCA	GCT	CAT	GGT	TTA	1799
Glu	Pro	Phe	Gly	Leu	Thr	Leu	Ile	Glu	Ala	Ala	Ala	His	Gly	Leu	
				620					625					630	
ccc	እጥር	Cuu	GCT	ACG	AAA	AAT	GGA	GGC	CCT	GTT	GAT	ATC	CAG	AGG	1844
			Ala												
PIO	Mec	***		635	-, -		•	•	640		-			645	
				000											
CEC	CTT	CAT	AAT	сст	СТТ	СТТ	GTG	GAT	CCT	CAT	GAG	CAG	CAG	TCT	1889
			Asn												
vaı	Den	ASP	NO!!	650	100				655					660	
				050											
	C CT	3 CM	GCT	መጥር	СТС	AAG	Стт	CTT	ССТ	GAT	AAG	CAA	СТА	TGG	1934
			Ala												
TIE	Ala	THE	MIG	665	Беа	цуз	Dea		670					675	
7.07	* * * *	mc C	CAG	CAA	дат	GGA	CTG	AAA	AAT	ATT	CAT	CTC	TAC	TCT	1979
			Gln												
THI	гуз	Cys	GIN	680				-1-	685				•	690	
				000		•			005						
		<b>~</b> > <b>~</b>	G 3 M	mcc	3 3 C	א כ א	ጥልር	רידים	ጥርጥ	CGA	מית	GCC	AGT	TCG	2024
			His												
Trp	Pro	GIU	HIS		гλг	IIII	TÄT	Deu		nrg	110		001	705	
				695					700					,03	
						mec		201	N	3 C C	CAM	C A A	GCC	Cum	2069
														CTT	2003
Arg	Gln	Arg	Gln		Glr	Trp	Gln	Arg		ser	ASD	1+ ] 11	GIŞ		
				710					715					720	

GAC	AAT	CAA	GAG	CCT	GAA	TCT	CCA	AGT	GAT	TCT	TTA	AGA	GAT	ATA	2114
Asp	Asn	Gln	Glu	Pro	Glu	Ser	Pro	Ser	Asp	Ser	Leu	Arg	Asp	Ile	
				725					730					735	
									CTC					•	2159
Lys	Asp	Ile	Ser	Leu	Asn	Leu	Glu	Val	Leu	Val	Arg	Pro	Glu	Lys	
				740					745					750	
									TTG						2204
Arg	Val	Lys	Thr		Lys	Ile	Leu	Gly	Leu	Met	Thr	Lys			
				755					760					765	
					mem	<b>m</b> 63	maa	mam			cmc.	G3.00		) mc	2240
									AAT						2249
ser	Arg	met	Leu		Cys	Ser	Trp	Ser	Asn 775	GIY	vaı	nis		мес 780	
				770					775					780	
СФФ	cee	AAG	ССТ	CGG	ጥጥር	тст	GAC	AAA	GTA	GAT	CAG	GCT	TCT	AGT	2294
									Val						
		270	•••	785					790					795	
AAA	TAT	CCA	GCA	TTT	AGG	AGG	AGA	AAA	CTT	ATA	TAT	GTT	ATT	GCT	2339
Lys	Tyr	Pro	Ala	Phe	Arg	Arg	Arg	Lys	Leu	Ile	Tyr	Val	Ile	Ala	
_				800					805					810	
GTA	GAC	GGG	GAT	TAT	GAA	GAT	GGA	CTT	TTT	GAT	ATT	GTT	CGG	AGG	2384
Val	Asp	Gly	Asp	Tyr	Glu	Asp	Gly	Leu	Phe	Asp	Ile	Val	Arg	Arg	
				815					820					825	

		GAT Asp													2429
				830					835				;	840	
		TTG													2474
Phe	Ile	Leu	Ser	Thr	Ser	Tyr	Ser	Met		Glu	Ile	Gln			
				845					850					855	
		TCA													2519
Leu	Leu	Ser	Lys		Phe	Asn	Leu	His		Phe	Asp	Ala			
maa	330	AGT	ccc	860 AGT	GAG.	ጥጥር	ጥልሮ	ጥልጥ	865 TCA	тст	ттс	AAC		870 GAG	2564
		Ser													
Cyc				875			-	•	880					885	
		AAT													2609
Glu	Ser	Asn	Ile	Ile	Ala	Asp	Ser	Asp	Tyr	His	Ser	His			
				890					895			<b></b>		900	2654
		TGG													2054
Tyr	Arg	Trp	GIÀ		Glu	GIĀ	reu	Arg	910	TIIL	Leu	Бец		915	
				905		•					C) A	CAA			2699
		TCC													2033
Ala	Ala	Ser	11e		GIU	гÀг	ASI	GIÀ	925	WOII	GIU	GIU		930	
				920					3 C J					., .,	

ATT	ACT	GAA	GAT	GAA	GAA	GTT	TCT	ACG	GGT	TAT	TGC	TTT	GCG	TTT	2744
Ile	Thr	Glu	Asp	Glu	Glu	Val	Ser	Thr	Gly	Tyr	Cys	Phe	Ala	Phe	
				935					940				9	945	
AAA	ATA	AAG	AAC	CAA	AAT	AAG	GTT	ĊCC	CCT	ACG	AAG	GAG	CTC	CGC	2789
Lys	Ile	Lys	Asn	Gln	Asn	Lys	Val	Pro	Pro	Thr	Lys	Glu	Leu	Arg	
				950					955				,	960	
•					•				•						
									TGC						2834
Lys	Ser	Met	Arg	Ile	Gln	Ala	Leu	Arg	Cys	His	Val	Ile	Tyr	Cys	
				965					970					975	
·															
									CCA						2879
Gln	Asn	Gly	Ser	Lys	Met	Asn	Val	Ile	Pro	Val	Leu	Ala			
				980					985					990	
															0004
									CGT						2924
Ser	Gln	Ala	Leu		Tyr	Leu	Tyr		Arg	Trp	GIÀ	Val		_	
				995				3	1000				1	005	
						amm	663	<b>C.</b> N. N.	mcm.	ccm	CAC	N C N	CNT	መአጥ	2969
									TGT						2909
Ser	Lys	Met			Phe	val	GIY		Cys	GIÀ	ASP	THE		020	
			:	1010					1015				1.	020	
			o==	CCC	<b>C</b> CC	CMC	Cym	<b>ת</b> ת ת	ACC	Cury	ג ידי <u>ג</u>	רתה	מממ	GGA	3014
															2014
Glu	Gjy	Leu			GΤĀ	val	піѕ		Thr	val	116	₩en		.035	
				1025					1030				_		

GTC	TCC	AAC	ACT	GCT	TTA	AGG	TCT	CTC	CAT	GCC	AAC	AGA	AGT	TAC	3055
Val	Ser	Asn	Thr	Ala	Leu	Arg	Ser	Leu	His	Ala	Asn	Arg	Ser	Tyr	
			1	1040				1	.045				1	050	
										•					
CCT	CTT	TCA	CAT	GTC	GTG	TCG	CTT	GAC	AGC	ccc	AAT	ATT	GGC	GAG	3104
Pro	Leu	Ser	His	Val	Val	Ser	Leu	Asp	Ser	Pro	Asn	Ile	Gly	Glu	
				1055					.060					065	
GTG	AGC	AAA	GGG	TGC	AGC	AGC	TCC	GAG	ATC	CAG	TCC	ATC	GTC	ACA	3149
			Gly												
		•		1070					.075					080	
AAA	CTC	TCC	AAA	GCT	TAA	TCAC	SATA	CT (	CTG	CTTTC	T T	rtgg	GTAA	G	3197
			Lys												
<b>-</b> ]				1085											
CAAC	GTT	rca '	rctt!	ATATO	SA T	rata:	CAT	A AG	ATAC	ATA	TAAC	GCAC	CTT		3247
••••															
Aጥጥር	GTA	AGT (	CAGT	CCA	ra ac	TAAT!	AATG	r AC	TTCAC	GAAC	CAC	AATA	CTT		3297
מממ	AGTTO	GT '	TCAG	ragto	GA T	ragro	CTCA	r aa:	TAAT	CATA	TAA!	TAC.	ACA		3347
	.0														
ሞርር	בכיתכי	בידים	ACTA	GTGG:	ra a	ratc:	raag(	C TC	AACA!	AATA	AGA:	rgta.	AAA		3391
100	,,,,,														
macr	ኮል ርጥን	מייה ו	GAAA:	rgaar	TT G	CTAG	CTGT:	r GA:	rcrc:	TTTC	CCT'	TAT'	TCT		344
100.	INGI		0.22.												
ר תי זא ני	יש ע ישינו	י סיחים	TTTC	רייראי	rc To	CATG	raaa.	A AC	AATT	TTCT	GAA	GGTG'	TAC		349
GIA.	IIMI.														
) CET	nanana.	TCC	CCTT	ል <b>ጥ</b> ልጥ:	ልጥ ሶሳ	יבייםי	ጉጥ Δ ጥኅ	ר ידכי	racti	ላ ጥጥጥ	TTT	GTTT	GTA		354
AGT"	1 1 1 1".	I CC	CC1 14	UIMI	71 C	LUIN.	. 4624 .								
		a cm	CTCA!	יייר איי	5C 74	בתכשי	ייזי ממיז	ממיד	ልጥል ልጥል	ccee	Стт	GCTA	ААТ		359
AGA	TAT	CLI	CTCH.	TCGW	JG M	orga.	- EMS-								

65

### ATAAAGCTTA TTCGAGTTAA AAAAAAAAA AAAAAAAA

3635

4. DNA sequence with the coding region for sucrose-synthase for the preparation of sugar beet with modified sucrose concentration, characterised in that the sequence has the following nucleotide sequence (Seq. ID No.4):

CT GCA GGA GGG AAA CAA ATT CTT AGC GAT GGC CCG TTT AGC GAA 0044
Ala Gly Gly Lys Gln Ile Leu Ser Asp Gly Pro Phe Ser Glu
5 10

GTT CTT AGG TCT GCT CAG GAA GCA ATA GTT GTT CCT CCC TTT GTT 0089

Val Leu Arg Ser Ala Gln Glu Ala Ile Val Val Pro Pro Phe Val

15 20 25

GCT ATA GCA GTC CGT CCA AGA CCT GGA GTT TGG GAA TAT GTT CGT 0134
Ala Ile Ala Val Arg Pro Arg Pro Gly Val Trp Glu Tyr Val Arg
30 35 40

GTT AAT GTC TCT GAA CTG AAT GTG GAG CAG CTA ACT GTG TCT GAG 0179
Val Asn Val Ser Glu Leu Asn Val Glu Gln Leu Thr Val Ser Glu
45 50 55

TAT CTC CAT TTC AAG GAA GAA CTT GTG GAT GGA AAG GCT GAT GAC

Tyr Leu His Phe Lys Glu Glu Leu Val Asp Gly Lys Ala Asp Asp

60

65

70

CAC TAT GTG CTT GAG CTT GAT TTC GAG CCT TTT AAT GAA TCA GTT 0269

His Tyr Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Glu Ser Val

75 80 85

CCA CGT CCA ACT CGC TCT TCA TCA ATT GGT AAT GGT GTT CAG TTC 0314

Pro Arg Pro Thr Arg Ser Ser Ile Gly Asn Gly Val Gln Phe
90 95 100

CTC AAT CGG CAC CTG TCA TCA AGC ATG TTC TGC AAC AAA GAT TO	GC 0359
Leu Asn Arg His Leu Ser Ser Met Phe Cys Asn Lys Asp C	
105 110 115	<del>-</del>
TTG GAG CCG TTA CTT GAT TTT CTT AGA GTG CAC AAA CAT AAA G	GA 0404
Leu Glu Pro Leu Leu Asp Phe Leu Arg Val His Lys His Lys-G	ly
120 125 130	
GTT GTC ATG ATG TTG AAT GAT CGG ATA CAG ACT ATC CAG CGT C	
Val Val Met Met Leu Asn Asp Arg Ile Gln Thr Ile Gln Arg L	eu
135 140 145	
CAG TCT GCA TTG TCT AAA GCT GAG GAT TAT CTT ATC AAA CTT C	CA 0494
Gln Ser Ala Leu Ser Lys Ala Glu Asp Tyr Leu Ile Lys Leu P	
150 155 160	
GCA GAT ACA CCT TAC TCT GAG TTC GAA TTT GTA ATC CAA GGT A	<b>T</b> G 0539
Ala Asp Thr Pro Tyr Ser Glu Phe Glu Phe Val Ile Gln Gly M	et
165 170 175	
GGT TTT GAA AGA GGC TGG GGT GAT ACT GCT GAA AGG GTT CTA G.	
Gly Phe Glu Arg Gly Trp Gly Asp Thr Ala Glu Arg Val Leu G	Iu
180 185 190	
•	
ATG ATG CAT CTA CTA GAT ATC CTT CAG GCT CCC GAT CCG T	CT 0629
Met Met His Leu Leu Asp Ile Leu Gln Ala Pro Asp Pro S	
195 200 205	

n-n	TTA	GAG	ACA	TTT	CTG	GGA	AGA	CTT	CCC	ATG	GTG	TTT	AAT	GTG	0674
Thr	Leu	Glu	Thr	Phe	Leu	Gly	Arg	Leu	Pro	Met	Val	Phe	Asn	Val	
210					215					220					
GTC	ATT	TTG	TCT	GTA	CAT	GGA	TAT	TTT	GGA	CAG	GCA	CAT	GTG	CTC	0719
Val	Ile	Leu	Ser	Val	His	Gly	Tyr	Phe	Gly.	_Gln-	Ala	His	Val	Leu	
225					230					235					
GGC	TTG	CCT	GAC	ACT	GGT	GGG	CAG	ATA	GTT.	TAT.	ATA.	CTT	GAC	CAA	0764
										Tyr					
240			-		245	_				250					
GTG	CGG	TCT	CTG	GAA	CAT	GAA	ATG	CTC	CAA	CGA	ATA	AAG	AAG	CAA	0809
Val	Arg	Ser	Leu	Glu	His	Glu	Met	Leu	Gln	Arg	Ile	Lys	Lys	Gln	
255	-				260					265					
GGA	CTA	GAT	GTG	ACT	CCT	AGA	ATT	CTT	ATC	GTG	A'GT	CGG	TTG	ATT	0854
										GTG Val					0854
															0854
Gly					Pro					Val					0854
Gly					Pro					Val					0854
Gly 270	Leu	Asp	Val	Thr	Pro 275	Arg	Ile	Leu	Ile	Val	Ser	Arg	Leu	Ile	0854
Gly 270 CCT	Leu GAC	Asp GCT	Val	Thr	Pro 275 ACC	Arg ACG	Ile	Leu	Ile	Val 280 CGT	Ser	Arg GAG	Leu AAA	Ile GTC	
Gly 270 CCT	Leu GAC	Asp GCT	Val	Thr	Pro 275 ACC	Arg ACG	Ile	Leu	Ile	Val 280	Ser	Arg GAG	Leu AAA	Ile GTC	
Gly 270 CCT Pro	Leu GAC	Asp GCT	Val	Thr	Pro 275 ACC Thr	Arg ACG	Ile	Leu	Ile	Val 280 CGT Arg	Ser	Arg GAG	Leu AAA	Ile GTC	
Gly 270 CCT Pro	Leu GAC	Asp GCT	Val	Thr	Pro 275 ACC Thr	Arg ACG	Ile	Leu	Ile	Val 280 CGT Arg	Ser	Arg GAG	Leu AAA	Ile GTC	
CCT Pro 285	Leu GAC Asp	Asp GCT Ala	Val AAA Lys	Thr GGG Gly	Pro 275 ACC Thr 290	Arg ACG Thr	Ile TGC Cys	Leu AAT Asn	CAA Gln	Val 280 CGT Arg	Ser ATG Met	Arg GAG Glu	Leu AAA Lys	Ile GTC Val	
Gly 270 CCT Pro 285	GAC Asp	GCT Ala	Val AAA Lys GAG	Thr GGG Gly CAT	Pro 275 ACC Thr 290	ACG Thr	TGC Cys	Leu AAT Asn	CAA Gln	Val 280 CGT Arg 295	Ser ATG Met	Arg GAG Glu TTC	AAA Lys CGA	Ile GTC Val	0899
Gly 270 CCT Pro 285	GAC Asp	GCT Ala	Val AAA Lys GAG	Thr GGG Gly CAT	Pro 275 ACC Thr 290	ACG Thr	TGC Cys	Leu AAT Asn	CAA Gln	Val 280 CGT Arg 295	Ser ATG Met	Arg GAG Glu TTC	AAA Lys CGA	Ile GTC Val	0899
CCT Pro 285	GAC Asp	GCT Ala	Val AAA Lys GAG	Thr GGG Gly CAT	Pro 275 ACC Thr 290 GCT Ala	ACG Thr	TGC Cys	Leu AAT Asn	CAA Gln	Val 280 CGT Arg 295 GTT Val	Ser ATG Met	Arg GAG Glu TTC	AAA Lys CGA	Ile GTC Val	0899

														maa	0000	
														TGG	0989	
Glu	Lys	Gly	Ile	Leu	Arg	Lys	Trp	Ile	Ser	Arg	Phe	Asp	Val	Trp		٠
315					320					325						
																•
				•	2-											
CCT	TAT	TTA	GAG	·ACC	TTC	ACT	GAG	GAT	GCA	GCT	GGT	GAA	ATT	ATT	1034	
Pro	Tvr	Leu	Glu	Thr	Phe	Thr	Glu	Asp	Ala	Ala	Gly	Glu	Ile	Ile		
330	4				335					340						
ccc	CAG	ጥጥር	CAG	GGT	CGT	CCA	GAT	CTG	ATA	ATT	GGC	AAC	TAC	AGC	1079	
			Gln													
_	Giu	Dea	G III	Cly	350	•				355			•			
345					330											
<b>-</b> 1.5			N CTI N	C TTITT	CCT	ጥርጥ	ጥጥ አ	ጥጥር	ጥርር	CAC	ΔΔΔ	ATG	GGT	GTC	1124	
			Ile													
-	GIY	ASI	116	٧aı	365	Ser	Dea	Дец	501	370	בינם		1			
360					205					370						
						<b>63.</b> M	663	mmc	C 2 C	***	3.00	አአሮ	ጥለጥ	CCA	1169	
														CCA		
Thr	Gln	Cys	Asn	Ile		H1S	Ala	Leu	GIU		THE	гÀг	171	PLO		
375					380					385						
			ATT												1214	
Asp	Ser	Asp	Ile	Tyr	Trp	Lys	Arg	Phe	Glu	Asp	Lys	Tyr	His	Phe		
390					395					400	•					
																•
					•	•										
TCG	TGT	CAA	TTT	TCA	GCT	GAC	TTG	ATG	GCA	ATG	AAT	CAT	GCT	GAT	1259	,
Ser	Cys	Gln	Phe	Ser	Ala	Asp	Leu	Met	Ala	Met	Asn	His	Ala	qzA		
405					410					415						

TTC	ATC	ATT	ACG	AGT	ACT	TAC	CAA	GAG	ATA	GCT	GGA	ACG	AAG	AAT	1304
Phe	Ile	Ile	Thr	Ser	Thr	Tyr	Gln	Glu	Ile	Ala	Gly	Thr	Lys	Asn	
420			•		425					430				•	
ACT	GTT	GGT	CAA	TAT	GAA	AGC	CAT	AAG	GCC	TTT	ACT	TTT	CCG	GGG	1349
Thr	Val	Gly	Gln	Tyr	Glu	Ser	His	Lys	Ala	Phe	Thr	Phe	Pro	Gly	
435					440					445					
CTG	TAT	CGG	GTG	GTT	CAC	GGG	ATT	GAT	GTC	TTT	GAT	ccc	AAG	TTT	1394
Leu	Tyr	Arg	Val	Val	His	Gly	Ile	Asp	Val	Phe	Asp	Pro	Lys	Phe	
450					455					460					
AAT	ATT	GTC	TCG	CCA	GGG	GCA	GAC	ATG	GCC	ATC	TAC	TTC	CCA	TTT	1439
Asn	Ile	Val	Ser	Pro	Gly	Ala	Asp	Met	Ala	Ile	Tyr	Phe	Pro	Phe	
465					470					475					
TCA	GAG	AAG	GAT	GTC	ACC	TGT	CTC	ACT	TCA	CTT	CAT	AGA	CTT	ATA	1484
Ser	Glu	Lys	Asp	Val	Thr	Cys	Leu	Thr	Ser	Leu	His	Arg	Leu	Ile	
480					485					490					
	CAG														1529
Glu	Gln	Leu	Leu	Phe	Lys	Pro	Glu	Gln	Asn	Glu	Glu	His	Ile	Gly	
495					500					505	•				
	TTA														1574
Val	Leu	Asp	Asp	Thr	Ser	Lys	Pro	Ile	Ile	Phe	Ser	Met	Ala	Arq	
510					515					520					

CTA	GAC	CGT	GTG	AAG	AAT	ATA	ACA	GGG	CTG	GTA	GAG	TGC	TAT	GGC	1619	
Leu	Asp	Arg	Val	Lys	Asn	Ile	Thr	Gly	Leu	Val	Glu	Cys	Tyr	GļY		
525					530					535						
AAG	ТАА	GCG	AAA	CTC	AGG	GAA	CTG	GCA	AAC	CTG	GTT	GTA	GTG	GCT	1664	
										Leu			•			
540			_1-		545					550						
540					3.13											
	m> 0	3300	~ » m	C TO N	222	AAG	Tree	አአጥ	GAC	AGG	GAG	GAA	እ ጥጥ	GCC	1709	
										Arg						
-	Tyr	ASN	Asp	vai		гÃ2	Ser	MSII	Asp	565	GIU.	GIU	116	nια		
555					560					262						
											<b></b>		mm »	262	1754	
										GAG					1754	-
Glu	Ile	Glu	Lys	Met		Arg	Leu	Ile	Gln	Glu	Tyr	Asn	Leu	Arg		
570					575					580						
										AAT					1799	
Gly	Gln	Phe	Arg	Trp	Ile	Ala	Ser	Gln	Thr	Asn	Arg	Val	Arg	Asn		
585					590					595						
GGT	GAA	CTC	TAT	CGC	TAC	ATT	TGT	GAC	AAA	GGA	GGT	ATT	TTT	GCG	1844	
Gly	Glu	Leu	Tyr	Arg	Tyr	Ile	Cys	Asp	Lys	Gly	Gly	Ile	Phe	Ala		
600					605					610						
																,
						•										
CAG	CCT	GCA	TTT	TAT	GAA	GCA	TTT	GGG	CTT	ACA	GTT	GTT	GAA	GCC	1889	J
										Thr						
615				-	620					625						

										TGC Cys 640					1934
										TTT Phe 655				CCA Pro	1979
TAT										GAA Glu					2024
660					665					670					
									Lys	ATC Ile 685					2069
									Trp	CAA Gln 700					2114
Arg					Ala					TTC Phe					2159
705 TCT	AAA	СТА	GAG	AGA	710 AGA	GAG	ACA	CGA	CGT	715 TAT	CTT	GAG	ATG	TTC	2204
Ser 720	Lys	Leu	Glu	Arg	Arg 725	Glu	Thr	Arg		Туг 730	Leu	Glu	Met	Phe	

														GCA	2249
Tyr	Ile	Leu	Lys	Phe	Arg	Asp	Leu	Ala			Val	Pro	Leu	Ala	
735					740					745					
א ר א	CDT	GAA	GAG	ርር የ	ጥርጥ	АСТ	АСТ	сат	GCA	ርጥጥ	GCG	ACA	ттс	CGT	2294
			Glu												
750					755					760					
													•		
GGA	CCT	TGA	ACG	CTGCT	rgc 1	TACI	rgago	T TO	CCAAC	STTGT	GT?	TAT	ATTA		2343
Gly	Pro	End													
<b>റ</b> ന്ന <b>െ</b> ന	הממטי	GG :	LATA!	י כיהכים	ים כי	יים ביי	מממ	AGC	ישרים	гсаа	СТАТ	ቦጥልርብ	ייאי		2393
CIGI	GAAL	igg 1	min	10101	ın o.		.0.22				01				
CTTC	TCTG	TG :	raaat	TAACO	A G	GTG	LAAAA	TG1	TAAT	ATTG	TTG	TGT	CTT		2443
GAAA	ACTO	AG :	rttgo	CTTTC	T T	rtta:	KATT?	A GTO	TATO	GACA	ATA	CTA	rca		2493
															25.40
TATA	ACGG	AT :	CTT	CAGTO	SA TO	CATAT	rcaa <i>i</i>	A'AC	TACI	rgac	CATO	GAAC	3'I"I'		2543
እ እጥር	ממממ:	ጥር (	GACAC	ברם מר	מי										2563
UW 1 C		(	mone		3										
	5.	I	eriv	ativ	es c	of DN	IA se	quen	ces	acco	rdin	g to	any	one	of

- 5. Derivatives of DNA sequences according to any one of claims 1 to 4 characterised in that these derivatives are obtained by exchange of single bases or by targeted or non-targeted mutagenesis.
- 6. Plasmids containing

5

a) a suitable promoter which ensures that the coding sequence meets a suitable time point or in the specified developments in the transgenic plant or in determined genes of transgenic plants;

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- at least one coding sequence according to claims 1 to 5, that
   i) is so coupled to the promoter that the formation of an RNA is allowed which is into a protein, whereby the protein demonstrates an enzymatic activity which leads to a modification of the sucrose
  - ii) which is so coupled to the promoter that the coding part is read, which leads to the formation of a so-called anti-sense RNA which under-expresses the formation of the protein coded from an endogenous gene in the plant, that is involved in the sucrose biosynthesis; and

concentration in the plant, or

- c) A non-coding termination sequence that contains the signal for the termination and polyadenylation of the transcript.
- 7. Use of the DNA-sequences according to any one of claims 1 to 6 for the preparation of sugar beet with changed sucrose concentration.
- 25 8. Use of the plasmids according to any one of claims 1-4 for the preparation of derivatives by targeted or non-targeted mutagenesis
- Sugar beet containing a DNA sequence according to
   any one of claims 1-5.